

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: August 17, 2002, 21:26:35 ; Search time 1890.87 Seconds
(without alignments)
254.544 Million cell updates/sec

Title: US-09-700-906A-3

Perfect score: 23
Sequence: 1 accaggcgtctcgtggccacat 23

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1797656 seqs, 10463268293 residues
Total number of hits satisfying chosen parameters: 708260

Minimum DB seq length: 0
Maximum DB seq length: 50

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : GenEmbl.*

- 1: gb_ba.*
- 2: gb_htg.*
- 3: gb_in.*
- 4: gb_om.*
- 5: gb_ov.*
- 6: gb_pat.*
- 7: gb_ph.*
- 8: gb_pl.*
- 9: gb_pr.*
- 10: gb_ro.*
- 11: gb_sts.*
- 12: gb_sy.*
- 13: gb_un.*
- 14: gb_vl.*
- 15: em_ba.*
- 16: em_fun.*
- 17: em_hum.*
- 18: em_in.*
- 19: em_mu.*
- 20: em_om.*
- 21: em_or.*
- 22: em_ov.*
- 23: em_pat.*
- 24: em_ph.*
- 25: em_pl.*
- 26: em_ro.*
- 27: em_sts.*
- 28: em_un.*
- 29: em_vl.*
- 30: em_htg_hum.*
- 31: em_htg_inv.*
- 32: em_htg_other.*
- 33: em_htgo_inv.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query	Score	Match	Length	DB	ID	Description
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AX009578	Sequence	23	100.0	1	23
AR044526	Sequence	23	63.5	2	14.6
AX350362	Sequence	37	61.7	3	14.2
I25110	Sequence 16	34	60.0	C 4	13.8
AR058898	Sequence	20	59.1	C 5	13.6
I36259	Sequence 4	20	59.1	C 6	13.6
A27934	Reshaped V1	45	59.1	7	13.6
AR050879	Sequence	45	59.1	8	13.6
I26287	Sequence 36	45	59.1	C 9	13.6
I51659	Sequence 6	45	59.1	C 10	13.6
A57109	Sequence 5	42	58.3	11	13.4
AX159478	Sequence	50	57.4	12	13.2
AX088381	Sequence	25	56.5	13	13
E04871	Synthetic D	29	56.5	C 14	13
AR051698	Sequence	27	54.8	C 15	12.6
I18231	Sequence 13	27	54.8	C 16	12.6
E40009	Drug contai	28	54.8	17	12.6
E40817	Humanized a	28	54.8	18	12.6
E43363	Humanized a	28	54.8	19	12.6
E17234	Linker. 7/1	34	54.8	C 20	12.6
I92662	Sequence 36	35	54.8	C 21	12.6
AX159452	Sequence	50	54.8	22	12.6
AR161561	Sequence	25	53.9	23	12.4
AR021325	Sequence	29	53.9	24	12.4
AX100907	Sequence	29	53.9	25	12.4
AX100909	Sequence	29	53.9	26	12.4
E65205	Method for	37	53.9	27	12.4
L08586	Human rear	39	53.9	28	12.4
AR136808	Sequence	40	53.9	29	12.4
BD000581	Amplifica	40	53.9	30	12.4
AR136807	Sequence	41	53.9	31	12.4
BD000580	Amplifica	41	53.9	32	12.4
AR136806	Sequence	42	53.9	33	12.4
BD000579	Amplifica	42	53.9	34	12.4
AX080147	Sequence	44	53.9	35	12.4
AX146582	Sequence	50	53.9	36	12.4
AR046856	Sequence	17	53.0	37	12.2
I53908	Sequence 16	17	53.0	38	12.2
AX295048	Sequence	20	53.0	39	12.2
AX095641	Sequence	21	53.0	40	12.2
AX067794	Sequence	24	53.0	C 41	12.2
AX290415	Sequence	24	53.0	C 42	12.2
A40417	Sequence 44	29	53.0	C 43	12.2
AR145384	Sequence	31	53.0	44	12.2
AR078093	Sequence	38	53.0	45	12.2
E35674	Detection o	38	53.0	46	12.2
I92644	Sequence 18	44	53.0	C 47	12.2
AR119756	Sequence	22	52.2	48	12
AR125453	Sequence	22	52.2	49	12
AR088241	Sequence	24	52.2	50	12
AR088239	Sequence	26	52.2	51	12
AX078736	Sequence	34	52.2	52	12
AX078737	Sequence	34	52.2	C 53	12
AR167245	Sequence	35	52.2	54	12
AR167244	Sequence	36	52.2	C 55	12
AR078292	Sequence	37	52.2	56	12
AR088238	Sequence	40	52.2	57	12
AR071086	Sequence	47	52.2	C 58	12
AR046854	Sequence	17	51.3	59	11.8
I53906	Sequence 16	17	51.3	60	11.8
AX349863	Sequence	28	51.3	61	11.8
AX203832	Sequence	29	51.3	C 62	11.8
AX254751	Sequence	29	51.3	63	11.8
AR100138	Sequence	31	51.3	C 64	11.8
AX212308	Sequence	31	51.3	65	11.8
E33819	Cell cycle	32	51.3	C 66	11.8
AX149519	Sequence	37	51.3	C 67	11.8
AX191411	Sequence	38	51.3	68	11.8
A84870	Sequence 19	39	51.3	69	11.8
AR144841	Sequence	39	51.3	70	11.8
AX006396	Sequence	39	51.3	71	11.8
AX015881	Sequence	39	51.3	72	11.8
AX191928	Sequence	39	51.3	73	11.8

74	11.8	51.3	39	6	AX286786	Sequence	AX286786	Sequence	147	11.4	49.6	30	6	I62803	Sequence 6
75	11.8	51.3	40	6	AR129812	Sequence	AR129812	Sequence	c 148	11.4	49.6	30	6	I3496	Sequence 5
c 76	11.8	51.3	40	6	AR148816	Sequence	AR148816	Sequence	149	11.4	49.6	30	6	I3497	Sequence 6
77	11.8	51.3	40	6	AX098436	Sequence	AX098436	Sequence	150	11.4	49.6	31	6	AR119396	Sequence
78	11.8	51.3	40	6	AX189547	Sequence	AX189547	Sequence	c 151	11.4	49.6	31	6	AX248074	Sequence
79	11.8	51.3	40	6	AX189681	Sequence	AX189681	Sequence	152	11.4	49.6	31	6	AX248912	Sequence
80	11.8	51.3	42	6	AR061496	Sequence	AR061496	Sequence	153	11.4	49.6	32	6	AX15517	Sequence
81	11.8	51.3	42	6	AR108395	Sequence	AR108395	Sequence	154	11.4	49.6	32	6	AX15522	Sequence
82	11.8	51.3	42	6	I16352	Sequence 17	I16352	Sequence 17	c 155	11.4	49.6	32	6	AR043550	Sequence
83	11.8	51.3	42	6	I66838	Sequence 17	I66838	Sequence 17	c 156	11.4	49.6	32	6	AR151642	Sequence
84	11.8	51.3	42	6	I84932	Sequence 17	I84932	Sequence 17	c 157	11.4	49.6	32	6	AR156798	Sequence
85	11.8	51.3	43	14	D88708	Sequence	D88708	Sequence	c 158	11.4	49.6	32	6	AX078819	Sequence
86	11.8	51.3	43	14	D88712	Sequence	D88712	Sequence	c 159	11.4	49.6	33	6	AX078820	Sequence
87	11.8	51.3	43	14	D88718	Sequence	D88718	Sequence	160	11.4	49.6	33	6	AX078820	Sequence
88	11.8	51.3	43	14	D88728	Sequence	D88728	Sequence	c 161	11.4	49.6	33	9	HS8TCR	Sequence
c 89	11.8	51.3	45	6	AX158327	Sequence	AX158327	Sequence	c 162	11.4	49.6	36	6	AX085547	Sequence
c 90	11.8	51.3	45	6	AX158328	Sequence	AX158328	Sequence	c 163	11.4	49.6	36	6	AR062968	Sequence
c 91	11.8	51.3	48	6	I92642	Sequence 16	I92642	Sequence 16	164	11.4	49.6	38	6	AX015886	Sequence
92	11.8	51.3	50	6	AR151515	Sequence	AR151515	Sequence	165	11.4	49.6	38	6	AX250339	Sequence
c 93	11.8	51.3	50	6	AR151519	Sequence	AR151519	Sequence	166	11.4	49.6	41	6	AR135731	Sequence
c 94	11.6	50.4	18	6	AR106852	Sequence	AR106852	Sequence	167	11.4	49.6	41	6	AX260004	Sequence
c 95	11.6	50.4	20	6	AX295738	Sequence	AX295738	Sequence	c 168	11.4	49.6	42	6	AX184285	Sequence
c 96	11.6	50.4	22	6	AX297426	Sequence	AX297426	Sequence	169	11.4	49.6	44	6	AR160602	Sequence
c 97	11.6	50.4	22	6	AR005278	Sequence	AR005278	Sequence	170	11.4	49.6	45	6	AX250698	Sequence
c 98	11.6	50.4	22	6	I90755	Sequence 4	I90755	Sequence 4	c 171	11.4	49.6	45	6	AX250698	Sequence
c 99	11.6	50.4	24	6	AX291105	Sequence	AX291105	Sequence	c 172	11.4	49.6	45	9	HUMTCCVJ45	Sequence
c 100	11.6	50.4	24	6	AX292793	Sequence	AX292793	Sequence	c 173	11.4	49.6	50	6	AX156994	Sequence
c 101	11.6	50.4	27	6	AX316328	Sequence	AX316328	Sequence	c 174	11.4	49.6	50	6	AX165817	Sequence
102	11.6	50.4	27	6	AX350075	Sequence	AX350075	Sequence	c 175	11.4	49.6	50	6	E59808	Sequence
103	11.6	50.4	28	6	AR090568	Sequence	AR090568	Sequence	c 176	11.2	48.7	18	6	E67603	Sequence 23
104	11.6	50.4	30	6	AX349879	Sequence	AX349879	Sequence	c 177	11.2	48.7	18	6	AR061025	Sequence
c 105	11.6	50.4	31	6	AX248163	Sequence	AX248163	Sequence	c 178	11.2	48.7	18	6	AR089741	Sequence
106	11.6	50.4	33	6	AR004409	Sequence	AR004409	Sequence	c 179	11.2	48.7	18	6	AR106896	Sequence
107	11.6	50.4	33	6	AR097201	Sequence	AR097201	Sequence	c 180	11.2	48.7	18	6	AR106931	Sequence
108	11.6	50.4	33	6	AR130699	Sequence	AR130699	Sequence	c 181	11.2	48.7	18	6	AX018741	Sequence
109	11.6	50.4	33	6	AR172048	Sequence	AR172048	Sequence	c 182	11.2	48.7	20	6	E29855	Sequence
110	11.6	50.4	33	6	AX280546	Sequence	AX280546	Sequence	c 183	11.2	48.7	20	6	E40795	Sequence
111	11.6	50.4	33	6	AX280551	Sequence	AX280551	Sequence	184	11.2	48.7	21	6	AX110191	Sequence
112	11.6	50.4	33	6	I82884	Sequence 63	I82884	Sequence 63	185	11.2	48.7	22	6	AR010210	Sequence
113	11.6	50.4	36	6	AX010671	Sequence	AX010671	Sequence	c 186	11.2	48.7	22	6	BD000134	Sequence
114	11.6	50.4	37	6	I65466	Sequence 2	I65466	Sequence 2	c 187	11.2	48.7	22	6	E03474	Sequence
115	11.6	50.4	38	6	BD003026	Design, C	BD003026	Design, C	188	11.2	48.7	22	6	I43326	Sequence 8
116	11.6	50.4	38	6	I34354	Sequence 53	I34354	Sequence 53	c 189	11.2	48.7	22	6	I95829	Sequence 8
117	11.6	50.4	40	6	I15926	Sequence 27	I15926	Sequence 27	c 190	11.2	48.7	23	6	AR091127	Sequence
118	11.6	50.4	40	6	I96125	Sequence 27	I96125	Sequence 27	c 191	11.2	48.7	24	6	AR125119	Sequence
119	11.6	50.4	43	6	AX146617	Sequence	AX146617	Sequence	c 192	11.2	48.7	24	6	AX288529	Sequence
120	11.6	50.4	50	6	AR054842	Sequence	AR054842	Sequence	c 193	11.2	48.7	24	6	AX290222	Sequence
121	11.6	50.4	50	6	AR066107	Sequence	AR066107	Sequence	c 194	11.2	48.7	26	6	AX010777	Sequence
122	11.6	50.4	50	9	HSHLA1A3	Sequence	HSHLA1A3	Sequence	c 195	11.2	48.7	26	6	AX010784	Sequence
c 123	11.6	50.4	50	9	HUMTCCRVJ41	Sequence	HUMTCCRVJ41	Sequence	c 196	11.2	48.7	26	6	AX081476	Sequence
c 124	11.4	49.6	17	6	AR104206	Sequence	AR104206	Sequence	c 197	11.2	48.7	27	6	E25836	Sequence
125	11.4	49.6	19	6	AX129907	Sequence	AX129907	Sequence	c 198	11.2	48.7	28	6	AX006923	Sequence
126	11.4	49.6	22	6	A84871	Sequence 20	A84871	Sequence 20	c 199	11.2	48.7	29	6	AX286740	Sequence
127	11.4	49.6	22	6	AR144842	Sequence	AR144842	Sequence	c 200	11.2	48.7	30	6	AX107511	Sequence
128	11.4	49.6	22	6	AR176149	Sequence	AR176149	Sequence	c 201	11.2	48.7	30	6	AX107535	Sequence
129	11.4	49.6	22	6	AX006398	Sequence	AX006398	Sequence	c 202	11.2	48.7	31	6	AR083549	Sequence
130	11.4	49.6	22	6	AX015883	Sequence	AX015883	Sequence	c 203	11.2	48.7	36	6	E40784	Sequence
131	11.4	49.6	22	6	AX015888	Sequence	AX015888	Sequence	204	11.2	48.7	38	6	AR063818	Sequence
132	11.4	49.6	22	6	AX191185	Sequence	AX191185	Sequence	c 205	11.2	48.7	39	6	I15928	Sequence 29
133	11.4	49.6	22	6	AX191412	Sequence	AX191412	Sequence	c 206	11.2	48.7	39	6	I15950	Sequence 51
134	11.4	49.6	22	6	AX191929	Sequence	AX191929	Sequence	c 207	11.2	48.7	39	6	I96127	Sequence 29
135	11.4	49.6	22	6	AX286788	Sequence	AX286788	Sequence	208	11.2	48.7	39	6	I96149	Sequence 51
136	11.4	49.6	24	6	AX291968	Sequence	AX291968	Sequence	209	11.2	48.7	40	6	I15944	Sequence 45
137	11.4	49.6	25	6	AX052680	Sequence	AX052680	Sequence	210	11.2	48.7	40	6	I15949	Sequence 50
c 138	11.4	49.6	26	6	AR091156	Sequence	AR091156	Sequence	211	11.2	48.7	40	6	I96143	Sequence 45
c 139	11.4	49.6	27	6	AR021326	Sequence	AR021326	Sequence	c 212	11.2	48.7	40	6	I96148	Sequence 50
c 140	11.4	49.6	27	6	E59887	Sequence	E59887	Sequence	c 213	11.2	48.7	42	6	AX300775	Sequence
141	11.4	49.6	27	6	AX109646	Sequence	AX109646	Sequence	c 214	11.2	48.7	42	6	AX300776	Sequence
142	11.4	49.6	28	6	AR176155	Sequence	AR176155	Sequence	c 215	11.2	48.7	43	6	AR100960	Sequence
143	11.4	49.6	28	6	AX191195	Sequence	AX191195	Sequence	c 216	11.2	48.7	45	9	HSAT278904	Sequence
144	11.4	49.6	28	6	AX191214	Sequence	AX191214	Sequence	c 217	11.2	48.7	48	9	HSU14058	Sequence
145	11.4	49.6	29	6	A97412	Sequence 2	A97412	Sequence 2	c 218	11.2	48.7	50	6	E16533	Sequence
c 146	11.4	49.6	30	6	I62802	Sequence 5	I62802	Sequence 5	c 219	11	47.8	19	6	AR139539	Sequence

220	11	47.8	21	6	AX095679 Sequence	AX095679 Sequence	c 293	10.8	47.0	24	6	A57385 Sequence 22
221	11	47.8	23	6	AR088242 Sequence	AR088242 Sequence	c 294	10.8	47.0	24	6	AR028445 Sequence
c-222	11	47.8	24	6	A92197 Sequence 31	A92197 Sequence 31	c 295	10.8	47.0	24	6	AR075384 Sequence
c 223	11	47.8	24	6	BD009172 Herbicide	BD009172 Herbicide	c 296	10.8	47.0	24	6	AX015220 Sequence
224	11	47.8	25	6	A48832 Sequence 24	A48832 Sequence 24	c 297	10.8	47.0	24	6	AX030702 Sequence
225	11	47.8	25	6	AX279054 Sequence	AX279054 Sequence	c 298	10.8	47.0	24	6	AX055030 Sequence
226	11	47.8	26	6	AR019480 Sequence	AR019480 Sequence	c 299	10.8	47.0	24	6	AX166504 Sequence
227	11	47.8	26	6	AR029003 Sequence	AR029003 Sequence	c 300	10.8	47.0	24	6	AX174822 Sequence
228	11	47.8	26	6	AR065941 Sequence	AR065941 Sequence	c 301	10.8	47.0	24	6	AX175503 Sequence
229	11	47.8	26	6	AX023675 Sequence	AX023675 Sequence	c 302	10.8	47.0	24	6	AX175511 Sequence
230	11	47.8	27	6	AR000011 Sequence	AR000011 Sequence	c 303	10.8	47.0	24	6	AX288328 Sequence
231	11	47.8	27	6	AR006779 Sequence	AR006779 Sequence	c 304	10.8	47.0	24	6	AX289475 Sequence
232	11	47.8	27	6	AR015967 Sequence	AR015967 Sequence	c 305	10.8	47.0	24	6	AX289529 Sequence
233	11	47.8	27	6	AR060924 Sequence	AR060924 Sequence	c 306	10.8	47.0	24	6	AX290618 Sequence
234	11	47.8	27	6	AR135387 Sequence	AR135387 Sequence	c 307	10.8	47.0	24	6	AX291134 Sequence
235	11	47.8	27	6	AX032419 Sequence	AX032419 Sequence	c 308	10.8	47.0	24	6	AX291661 Sequence
c 236	11	47.8	27	6	AX034682 Sequence	AX034682 Sequence	c 309	10.8	47.0	24	6	AX291773 Sequence
c 237	11	47.8	27	6	AX343650 Sequence	AX343650 Sequence	c 310	10.8	47.0	24	6	AX291849 Sequence
238	11	47.8	27	6	BD004718 Sequence	BD004718 Chimeric	c 311	10.8	47.0	24	6	AX298290 Sequence
239	11	47.8	27	6	I40980 Sequence 9	I40980 Sequence 9	c 312	10.8	47.0	24	6	AX300720 Sequence
240	11	47.8	27	6	I71291 Sequence 29	I71291 Sequence 29	c 313	10.8	47.0	24	6	AX300929 Sequence
241	11	47.8	28	6	E40799 Antihuman F	E40799 Antihuman F	c 314	10.8	47.0	24	6	BD006697 Transport
c 242	11	47.8	29	6	AX104378 Sequence	AX104378 Sequence	c 315	10.8	47.0	24	6	E14845 PCR primer.
c 243	11	47.8	29	6	AX355803 Sequence	AX355803 Sequence	c 316	10.8	47.0	25	6	AX349971 Sequence
244	11	47.8	30	6	A22349 H.sapiens H	A22349 H.sapiens H	c 317	10.8	47.0	26	6	AR090256 Sequence
c 245	11	47.8	30	6	AR041112 Sequence	AR041112 Sequence	c 318	10.8	47.0	26	6	E17233 Linker. 7/1
c 246	11	47.8	30	6	AR066006 Sequence	AR066006 Sequence	c 319	10.8	47.0	27	6	AR000575 Sequence
c 247	11	47.8	30	6	AR072748 Sequence	AR072748 Sequence	c 320	10.8	47.0	27	6	AX063382 Sequence
248	11	47.8	30	10	S86291 TCR V beta	S86291 TCR V beta	c 321	10.8	47.0	27	6	BD003627 A polynuc
249	11	47.8	31	6	AX248477 Sequence	AX248477 Sequence	c 322	10.8	47.0	28	6	AR049468 Sequence
250	11	47.8	31	6	AX248707 Sequence	AX248707 Sequence	c 323	10.8	47.0	28	6	AR051619 Sequence
251	11	47.8	31	6	AX248814 Sequence	AX248814 Sequence	c 324	10.8	47.0	29	6	A57691 Sequence 1
c 252	11	47.8	31	6	E02911 oligonucleo	E02911 oligonucleo	c 325	10.8	47.0	29	6	A76939 Sequence 1
253	11	47.8	32	6	AR125498 Sequence	AR125498 Sequence	c 326	10.8	47.0	29	6	AR070077 Sequence
c 254	11	47.8	32	6	AX093107 Sequence	AX093107 Sequence	c 327	10.8	47.0	30	6	A14220 oligonucleo
c 255	11	47.8	33	6	AR004384 Sequence	AR004384 Sequence	c 328	10.8	47.0	30	6	AR063744 Sequence
256	11	47.8	33	6	AR097175 Sequence	AR097175 Sequence	c 329	10.8	47.0	30	6	AR084491 Sequence
c 257	11	47.8	33	6	AR125497 Sequence	AR125497 Sequence	c 330	10.8	47.0	30	6	AR107271 Sequence
258	11	47.8	33	6	AR130673 Sequence	AR130673 Sequence	c 331	10.8	47.0	30	6	AR107272 Sequence
259	11	47.8	33	6	AR172022 Sequence	AR172022 Sequence	c 332	10.8	47.0	30	6	AR159571 Sequence
c 260	11	47.8	33	6	AR134751 Sequence	AR134751 Sequence	c 333	10.8	47.0	30	6	AR172390 Sequence
261	11	47.8	33	6	I82859 Sequence 38	I82859 Sequence 38	c 334	10.8	47.0	30	6	I30107 Sequence 29
c 262	11	47.8	34	6	A93643 Sequence 2	A93643 Sequence 2	c 335	10.8	47.0	31	6	AR071456 Sequence
c 263	11	47.8	34	6	AR176284 Sequence	AR176284 Sequence	c 336	10.8	47.0	31	6	AX249666 Sequence
264	11	47.8	35	6	I40076 Sequence 35	I40076 Sequence 35	c 337	10.8	47.0	31	6	AX280677 Sequence
c 265	11	47.8	35	6	I40078 Sequence 37	I40078 Sequence 37	c 338	10.8	47.0	31	6	AX280678 Sequence
c 266	11	47.8	35	9	S72578 TCR delta =	S72578 TCR delta =	c 339	10.8	47.0	31	6	BD002908 Gene comp
c 267	11	47.8	36	6	A63365 Sequence 20	A63365 Sequence 20	c 340	10.8	47.0	31	6	I41399 Sequence 2
c 268	11	47.8	36	6	AX092228 Sequence	AX092228 Sequence	c 341	10.8	47.0	32	6	AX280679 Sequence
c 269	11	47.8	36	6	AX224672 Sequence	AX224672 Sequence	c 342	10.8	47.0	32	6	AX280680 Sequence
270	11	47.8	40	6	AR078066 Sequence	AR078066 Sequence	c 343	10.8	47.0	32	6	E36188 Upstream re
271	11	47.8	40	6	E35647 Sequence o	E35647 Detection o	c 344	10.8	47.0	33	6	AR071445 Sequence
272	11	47.8	41	6	AR078065 Sequence	AR078065 Sequence	c 345	10.8	47.0	33	6	AX317353 Sequence
273	11	47.8	41	6	E35646 Detection o	E35646 Detection o	c 346	10.8	47.0	33	6	AX317354 Sequence
c 274	11	47.8	42	6	AX044068 Sequence	AX044068 Sequence	c 347	10.8	47.0	35	6	AR099775 Sequence
c 275	11	47.8	45	6	A68107 Sequence 16	A68107 Sequence 16	c 348	10.8	47.0	36	6	AX077721 Sequence
c 276	11	47.8	45	6	A68111 Sequence 20	A68111 Sequence 20	c 349	10.8	47.0	36	6	AX136876 Sequence
277	11	47.8	45	6	E22037 Seven-pass	E22037 Seven-pass	c 350	10.8	47.0	36	6	AX136878 Sequence
c 278	11	47.8	47	6	AX044058 Sequence	AX044058 Sequence	c 351	10.8	47.0	36	6	E27482 Novel Dnae
c 279	11	47.8	48	6	AR024316 Sequence	AR024316 Sequence	c 352	10.8	47.0	37	6	AX211299 Sequence
280	11	47.8	48	6	AR045169 Sequence	AR045169 Sequence	c 353	10.8	47.0	37	6	AX211300 Sequence
281	11	47.8	48	6	BD011393 Chimeric	BD011393 Chimeric	c 354	10.8	47.0	38	9	HUMTCRVJ40
282	11	47.8	48	6	E43863 Chimeric an	E43863 Chimeric an	c 355	10.8	47.0	39	6	AR001559 Sequence
c 283	11	47.8	49	6	I05520 Sequence 8	I05520 Sequence 8	c 356	10.8	47.0	39	6	AR086367 Sequence
c 284	10.8	47.0	19	6	AX129198 Sequence	AX129198 Sequence	c 357	10.8	47.0	39	6	AR104976 Sequence
c 285	10.8	47.0	20	6	AX201609 Sequence	AX201609 Sequence	c 358	10.8	47.0	39	6	AR145839 Sequence
c 286	10.8	47.0	20	6	AX253336 Sequence	AX253336 Sequence	c 359	10.8	47.0	39	6	E35283 Assay of Ch
c 287	10.8	47.0	20	6	AX292961 Sequence	AX292961 Sequence	c 360	10.8	47.0	40	6	A67373 Sequence 12
c 288	10.8	47.0	20	6	AX294855 Sequence	AX294855 Sequence	c 361	10.8	47.0	40	6	A90919 Sequence 26
c 289	10.8	47.0	20	6	AX296406 Sequence	AX296406 Sequence	c 362	10.8	47.0	40	6	AX202304 Sequence
290	10.8	47.0	20	6	I12670 Sequence 80	I12670 Sequence 80	c 363	10.8	47.0	40	6	I92643 Sequence 17
291	10.8	47.0	21	6	AR177624 Sequence	AR177624 Sequence	c 364	10.8	47.0	41	9	S81437 T cell anti
c 292	10.8	47.0	23	6	E07721 Primer. 9/1	E07721 Primer. 9/1	c 365	10.8	47.0	42	6	AR100925 Sequence

c 366	10.8	47.0	43	6	AX008489	Sequence	AX008489	Sequence	c 439	10.6	46.1	22	6	AR012666	Sequence	AR012666	Sequence
c 367	10.8	47.0	43	6	AX085142	Sequence	AX085142	Sequence	c 440	10.6	46.1	22	6	I25032	Sequence 6	I25032	Sequence 6
c 368	10.8	47.0	44	6	AX086375	Sequence	AX086375	Sequence	c 441	10.6	46.1	22	6	I30494	Sequence 6	I30494	Sequence 6
c 369	10.8	47.0	44	9	HUMFTBB	MI5899 Human nucle	MI5899	Human nucle	c 442	10.6	46.1	22	6	I72556	Sequence 5	I72556	Sequence 5
c 370	10.8	47.0	45	6	AR021427	Sequence	AR021427	Sequence	c 443	10.6	46.1	23	6	AR051700	Sequence	AR051700	Sequence
c 371	10.8	47.0	45	6	AR021428	Sequence	AR021428	Sequence	c 444	10.6	46.1	23	6	AR069972	Sequence	AR069972	Sequence
c 372	10.8	47.0	45	6	AR042989	Sequence	AR042989	Sequence	c 445	10.6	46.1	23	6	AX322619	Sequence	AX322619	Sequence
c 373	10.8	47.0	45	6	AR042990	Sequence	AR042990	Sequence	c 446	10.6	46.1	23	6	I18233	Sequence 15	I18233	Sequence 15
c 374	10.8	47.0	45	6	AR086374	Sequence	AR086374	Sequence	c 447	10.6	46.1	24	6	AX290711	Sequence	AX290711	Sequence
c 375	10.8	47.0	45	6	AR117917	Sequence	AR117917	Sequence	c 448	10.6	46.1	24	6	AX291106	Sequence	AX291106	Sequence
c 376	10.8	47.0	45	6	AR161323	Sequence	AR161323	Sequence	c 449	10.6	46.1	24	6	AX291628	Sequence	AX291628	Sequence
c 377	10.8	47.0	45	6	AR161324	Sequence	AR161324	Sequence	c 450	10.6	46.1	24	6	E13447	PCR primer	E13447	PCR primer
c 378	10.8	47.0	45	6	I43968	Sequence 59	I43968	Sequence 59	c 451	10.6	46.1	25	6	AR051699	Sequence	AR051699	Sequence
c 379	10.8	47.0	45	6	I43969	Sequence 60	I43969	Sequence 60	c 452	10.6	46.1	25	6	AX039274	Sequence	AX039274	Sequence
c 380	10.8	47.0	45	6	I62980	Sequence 10	I62980	Sequence 10	c 453	10.6	46.1	25	6	I18232	Sequence 14	I18232	Sequence 14
c 381	10.8	47.0	45	6	I62981	Sequence 10	I62981	Sequence 10	c 454	10.6	46.1	26	6	AR106358	Sequence	AR106358	Sequence
c 382	10.8	47.0	45	6	I88733	Sequence 10	I88733	Sequence 10	c 455	10.6	46.1	27	6	AR07708	Synthetic n	AR07708	Synthetic n
c 383	10.8	47.0	45	6	I88734	Sequence 10	I88734	Sequence 10	c 456	10.6	46.1	27	6	AI0007	Nucleotide	AI0007	Nucleotide
c 384	10.8	47.0	46	6	A42682	Sequence 14	A42682	Sequence 14	c 457	10.6	46.1	27	6	AR1445	Sequence 8	AR1445	Sequence 8
c 385	10.8	47.0	46	6	A74862	Sequence 54	A74862	Sequence 54	c 458	10.6	46.1	27	6	AR1614	Sequence 8	AR1614	Sequence 8
c 386	10.8	47.0	46	6	A77841	Sequence 54	A77841	Sequence 54	c 459	10.6	46.1	27	6	AR017903	Sequence	AR017903	Sequence
c 387	10.8	47.0	46	6	AR043537	Sequence	AR043537	Sequence	c 460	10.6	46.1	27	6	AR024195	Sequence	AR024195	Sequence
c 388	10.8	47.0	46	6	AR063856	Sequence	AR063856	Sequence	c 461	10.6	46.1	27	6	BD005344	Enhanced	BD005344	Enhanced
c 389	10.8	47.0	46	6	AR075820	Sequence	AR075820	Sequence	c 462	10.6	46.1	27	6	I15110	Sequence 13	I15110	Sequence 13
c 390	10.8	47.0	46	6	AR098732	Sequence	AR098732	Sequence	c 463	10.6	46.1	29	6	AX351506	Sequence	AX351506	Sequence
c 391	10.8	47.0	46	6	AR112324	Sequence	AR112324	Sequence	c 464	10.6	46.1	30	6	AX047007	Sequence	AX047007	Sequence
c 392	10.8	47.0	46	6	E30453	E30453 Method for	E30453	Method for	c 465	10.6	46.1	30	6	AX047016	Sequence	AX047016	Sequence
c 393	10.8	47.0	46	6	E32363	E32363 Method for	E32363	Method for	c 466	10.6	46.1	30	10	MHNF113B	X66552 Mus muscula	X66552	Mus muscula
c 394	10.8	47.0	46	6	E33634	Detection o	E33634	Detection o	c 467	10.6	46.1	31	6	AX001316	Sequence	AX001316	Sequence
c 395	10.8	47.0	46	6	E35691	E35691 Detection a	E35691	Detection a	c 468	10.6	46.1	31	6	E36252	Human semap	E36252	Human semap
c 396	10.8	47.0	46	6	I87188	Sequence 14	I87188	Sequence 14	c 469	10.6	46.1	32	6	AR075029	Sequence	AR075029	Sequence
c 397	10.8	47.0	47	10	S82866S2	S82867 Apod-apolip	S82867	Apod-apolip	c 470	10.6	46.1	32	6	AR118493	Sequence	AR118493	Sequence
c 398	10.8	47.0	48	6	AR049475	Sequence	AR049475	Sequence	c 471	10.6	46.1	33	6	AR064939	Sequence	AR064939	Sequence
c 399	10.8	47.0	48	6	AR051626	Sequence	AR051626	Sequence	c 472	10.6	46.1	33	6	AR097192	Sequence	AR097192	Sequence
c 400	10.8	47.0	48	9	HSU14064	Human T cel	U14064	Human T cel	c 473	10.6	46.1	33	6	AR130690	Sequence	AR130690	Sequence
c 401	10.8	47.0	49	6	AX019736	Sequence	AX019736	Sequence	c 474	10.6	46.1	33	6	AR172039	Sequence	AR172039	Sequence
c 402	10.8	47.0	50	6	AI4174	AI4174 vectorette	AI4174	vectorette	c 475	10.6	46.1	35	6	AR043567	Sequence	AR043567	Sequence
c 403	10.8	47.0	50	6	AI4176	AI4176 vectorette	AI4176	vectorette	c 476	10.6	46.1	35	6	AX058076	Sequence	AX058076	Sequence
c 404	10.8	47.0	50	6	AI4178	AI4178 vectorette	AI4178	vectorette	c 477	10.6	46.1	36	6	A33740	Synthetic D	A33740	Synthetic D
c 405	10.8	47.0	50	6	AI4198	AI4198 specific ve	AI4198	specific ve	c 478	10.6	46.1	36	6	A33741	Synthetic D	A33741	Synthetic D
c 406	10.8	47.0	50	6	AR032767	Sequence	AR032767	Sequence	c 479	10.6	46.1	36	6	AR068333	Sequence	AR068333	Sequence
c 407	10.8	47.0	50	6	AX000366	Sequence	AX000366	Sequence	c 480	10.6	46.1	36	6	AX019533	Sequence	AX019533	Sequence
c 408	10.8	47.0	50	6	AX000367	Sequence	AX000367	Sequence	c 481	10.6	46.1	36	6	AX268888	Sequence	AX268888	Sequence
c 409	10.8	47.0	50	6	AX160500	Sequence	AX160500	Sequence	c 482	10.6	46.1	36	6	AX268894	Sequence	AX268894	Sequence
c 410	10.8	47.0	50	6	AX199682	Sequence	AX199682	Sequence	c 483	10.6	46.1	36	6	AX317301	Sequence	AX317301	Sequence
c 411	10.8	47.0	50	6	E40785	E40785 Antihuman F	E40785	Antihuman F	c 484	10.6	46.1	36	6	AX317314	Sequence	AX317314	Sequence
c 412	10.8	47.0	50	6	I29507	I29507 Sequence 37	I29507	Sequence 37	c 485	10.6	46.1	36	6	AX317480	Sequence	AX317480	Sequence
c 413	10.8	47.0	50	6	I91181	Sequence 37	I91181	Sequence 37	c 486	10.6	46.1	36	6	I65465	Sequence 1	I65465	Sequence 1
c 414	10.6	46.1	18	6	AR052908	Sequence	AR052908	Sequence	c 487	10.6	46.1	38	6	A28707	Dia 5' prim	A28707	Dia 5' prim
c 415	10.6	46.1	18	6	AR054271	Sequence	AR054271	Sequence	c 488	10.6	46.1	38	6	I19043	Sequence 3	I19043	Sequence 3
c 416	10.6	46.1	18	6	AR054473	Sequence	AR054473	Sequence	c 489	10.6	46.1	39	6	AR004622	Sequence	AR004622	Sequence
c 417	10.6	46.1	18	6	AR163072	Sequence	AR163072	Sequence	c 490	10.6	46.1	39	6	I65468	Sequence 4	I65468	Sequence 4
c 418	10.6	46.1	18	6	E01966	E01966 Variant ind	E01966	Variant ind	c 491	10.6	46.1	40	6	AR004621	Sequence	AR004621	Sequence
c 419	10.6	46.1	18	6	I24671	I24671 Sequence 55	I24671	Sequence 55	c 492	10.6	46.1	40	6	AR105362	Sequence	AR105362	Sequence
c 420	10.6	46.1	18	6	I25268	I25268 Sequence 55	I25268	Sequence 55	c 493	10.6	46.1	40	6	AR135207	Sequence	AR135207	Sequence
c 421	10.6	46.1	19	6	AR157491	Sequence	AR157491	Sequence	c 494	10.6	46.1	40	6	AR135220	Sequence	AR135220	Sequence
c 422	10.6	46.1	19	6	AX166874	Sequence	AX166874	Sequence	c 495	10.6	46.1	40	6	AR146703	Sequence	AR146703	Sequence
c 423	10.6	46.1	20	6	AR050659	Sequence	AR050659	Sequence	c 496	10.6	46.1	40	6	AR146716	Sequence	AR146716	Sequence
c 424	10.6	46.1	20	6	AR124491	Sequence	AR124491	Sequence	c 497	10.6	46.1	40	6	AR152274	Sequence	AR152274	Sequence
c 425	10.6	46.1	20	6	AR126630	Sequence	AR126630	Sequence	c 498	10.6	46.1	40	6	AR152287	Sequence	AR152287	Sequence
c 426	10.6	46.1	20	6	AX056719	Sequence	AX056719	Sequence	c 499	10.6	46.1	40	6	AR157812	Sequence	AR157812	Sequence
c 427	10.6	46.1	20	6	AX295344	Sequence	AX295344	Sequence	c 500	10.6	46.1	40	6	AR157825	Sequence	AR157825	Sequence
c 428	10.6	46.1	20	6	AX295739	Sequence	AX295739	Sequence	c 501	10.6	46.1	42	6	AR154192	Sequence	AR154192	Sequence
c 429	10.6	46.1	20	6	E08449	E08449 DNA fragmen	E08449	DNA fragmen	c 502	10.6	46.1	42	6	AR175519	Sequence	AR175519	Sequence
c 430	10.6	46.1	20	6	E08910	E08910 Oligonucleo	E08910	Oligonucleo	c 503	10.6	46.1	42	6	AX268903	Sequence	AX268903	Sequence
c 431	10.6	46.1	20	6	E37917	E37917 Nucleic aci	E37917	Nucleic aci	c 504	10.6	46.1	42	6	AX268907	Sequence	AX268907	Sequence
c 432	10.6	46.1	20	6	I12598	I12598 Sequence 8	I12598	Sequence 8	c 505	10.6	46.1	42	9	HUMTCCV36	L39503 Homo saplen	L39503	Homo saplen
c 433	10.6	46.1	21	6	AR069973	Sequence	AR069973	Sequence	c 506	10.6	46.1	45	6	AR007208	Sequence	AR007208	Sequence
c 434	10.6	46.1	21	6	AX095147	Sequence	AX095147	Sequence	c 507	10.6	46.1	45	6	AR048111	Sequence	AR048111	Sequence
c 435	10.6	46.1	21	6	AX096280	Sequence	AX096280	Sequence	c 508	10.6	46.1	45	6	AR054215	Sequence	AR054215	Sequence
c 436	10.6	46.1	21	6	AX201232	Sequence	AX201232	Sequence	c 509	10.6	46.1	45	6	AR063976	Sequence	AR063976	Sequence
c 437	10.6	46.1	22	6	A87888	Sequence 36	A87888	Sequence 36	c 510	10.6	46.1	45	6	AR107743	Sequence	AR107743	Sequence
c 438	10.6	46.1	22	6	A89855	Sequence 36	A89855	Sequence 36	c 511	10.6	46.1	45	6	AR117920	Sequence	AR117920	Sequence

c 512	10.6	46.1	46	6	AR032532	AR032532 Sequence	c 585	10.4	45.2	27	6	E06045	E06045 Linker. 9/1
c 513	10.6	46.1	46	6	I29272	I29272 Sequence 14	c 586	10.4	45.2	27	6	I21793	I21793 Sequence 7
c 514	10.6	46.1	46	6	I90946	I90946 Sequence 14	c 587	10.4	45.2	27	6	I57362	I57362 Sequence 5
c 515	10.6	46.1	47	6	AR027754	AR027754 Sequence	c 588	10.4	45.2	27	6	I66408	I66408 Sequence 6
c 516	10.6	46.1	47	6	AR029158	AR029158 Sequence	c 589	10.4	45.2	27	6	I66409	I66409 Sequence 7
c 517	10.6	46.1	47	6	AR036542	AR036542 Sequence	c 590	10.4	45.2	28	6	AX280309	AX280309 Sequence
c 518	10.6	46.1	47	6	AR096075	AR096075 Sequence	c 591	10.4	45.2	29	6	AX022542	AX022542 Sequence
c 519	10.6	46.1	47	6	AR111942	AR111942 Sequence	c 592	10.4	45.2	29	6	AX022543	AX022543 Sequence
c 520	10.6	46.1	47	6	AR124839	AR124839 Sequence	c 593	10.4	45.2	29	6	AX175194	AX175194 Sequence
c 521	10.6	46.1	47	6	AR135287	AR135287 Sequence	c 594	10.4	45.2	29	6	AX280510	AX280510 Sequence
c 522	10.6	46.1	47	6	AR141340	AR141340 Sequence	c 595	10.4	45.2	29	6	E39279	E39279 Labeled pri
c 523	10.6	46.1	47	6	AR157495	AR157495 Sequence	c 596	10.4	45.2	29	6	E39280	E39280 Labeled pri
c 524	10.6	46.1	47	6	I31656	I31656 Sequence 7	c 597	10.4	45.2	30	6	AR051649	AR051649 Sequence
c 525	10.6	46.1	47	6	I41038	I41038 Sequence 7	c 598	10.4	45.2	30	6	AR124218	AR124218 Sequence
c 526	10.6	46.1	48	6	AX164151	AX164151 Sequence	c 599	10.4	45.2	30	6	AX151765	AX151765 Sequence
c 527	10.6	46.1	49	6	AX45046	AX45046 Sequence 21	c 600	10.4	45.2	30	6	AX350348	AX350348 Sequence
c 528	10.6	46.1	49	6	AR029662	AR029662 Sequence	c 601	10.4	45.2	30	6	BD005219	BD005219 Novel yea
c 529	10.6	46.1	49	6	I44605	I44605 Sequence 34	c 602	10.4	45.2	31	6	A75719	A75719 Sequence 9
c 530	10.6	46.1	49	6	I71010	I71010 Sequence 34	c 603	10.4	45.2	31	6	AX248383	AX248383 Sequence
c 531	10.4	45.2	13	6	AR136588	AR136588 Sequence	c 604	10.4	45.2	31	6	AX248866	AX248866 Sequence
c 532	10.4	45.2	15	6	AR033413	AR033413 Sequence	c 605	10.4	45.2	31	6	AX248867	AX248867 Sequence
c 533	10.4	45.2	15	6	AR113235	AR113235 Sequence	c 606	10.4	45.2	31	6	AX249286	AX249286 Sequence
c 534	10.4	45.2	15	6	I57642	I57642 Sequence 17	c 607	10.4	45.2	31	6	AX249318	AX249318 Sequence
c 535	10.4	45.2	18	6	AR048722	AR048722 Sequence	c 608	10.4	45.2	31	6	BD002553	BD002553 Gene comp
c 536	10.4	45.2	19	6	AX278625	AX278625 Sequence	c 609	10.4	45.2	32	6	A39467	A39467 Sequence 26
c 537	10.4	45.2	20	6	AR011700	AR011700 Sequence	c 610	10.4	45.2	32	6	A98587	A98587 Sequence 12
c 538	10.4	45.2	20	6	AR092300	AR092300 Sequence	c 611	10.4	45.2	32	6	A98587	A98587 Sequence 12
c 539	10.4	45.2	20	6	AR119517	AR119517 Sequence	c 612	10.4	45.2	32	6	AR001358	AR001358 Sequence
c 540	10.4	45.2	20	6	AR122434	AR122434 Sequence	c 613	10.4	45.2	32	6	AR028335	AR028335 Sequence
c 541	10.4	45.2	20	6	AX201713	AX201713 Sequence	c 614	10.4	45.2	32	6	AR044843	AR044843 Sequence
c 542	10.4	45.2	20	6	AX297314	AX297314 Sequence	c 615	10.4	45.2	32	6	AR044853	AR044853 Sequence
c 543	10.4	45.2	20	6	I33074	I33074 Sequence 10	c 616	10.4	45.2	32	6	AR052229	AR052229 Sequence
c 544	10.4	45.2	21	6	AR125499	AR125499 Sequence	c 617	10.4	45.2	32	6	AR052239	AR052239 Sequence
c 545	10.4	45.2	21	6	AX038334	AX038334 Sequence	c 618	10.4	45.2	32	6	AR070855	AR070855 Sequence
c 546	10.4	45.2	21	6	AX095982	AX095982 Sequence	c 619	10.4	45.2	32	6	AR078338	AR078338 Sequence
c 547	10.4	45.2	21	6	AX189549	AX189549 Sequence	c 620	10.4	45.2	32	6	AR085189	AR085189 Sequence
c 548	10.4	45.2	21	6	AX189683	AX189683 Sequence	c 621	10.4	45.2	32	6	AR138109	AR138109 Sequence
c 549	10.4	45.2	21	6	BD010972	BD010972 Novel phy	c 622	10.4	45.2	32	6	AR156444	AR156444 Sequence
c 550	10.4	45.2	22	6	AR173689	AR173689 Sequence	c 623	10.4	45.2	32	6	AX040345	AX040345 Sequence
c 551	10.4	45.2	22	6	AX038335	AX038335 Sequence	c 624	10.4	45.2	32	6	AX202204	AX202204 Sequence
c 552	10.4	45.2	22	6	AX107493	AX107493 Sequence	c 625	10.4	45.2	32	6	E13335	E13335 Primer. 6/1
c 553	10.4	45.2	22	6	E31632	E31632 Method for	c 626	10.4	45.2	32	6	E38136	E38136 Method for
c 554	10.4	45.2	22	6	E31642	E31642 Method for	c 627	10.4	45.2	32	6	I24933	I24933 Sequence 5
c 555	10.4	45.2	22	6	E31643	E31643 Method for	c 628	10.4	45.2	32	6	I33893	I33893 Sequence 1
c 556	10.4	45.2	23	6	AR078447	AR078447 Sequence	c 629	10.4	45.2	32	6	I33903	I33903 Sequence 11
c 557	10.4	45.2	23	6	AX038336	AX038336 Sequence	c 630	10.4	45.2	32	6	I35717	I35717 Sequence 6
c 558	10.4	45.2	24	6	A69677	A69677 Sequence 7	c 631	10.4	45.2	32	23	E11416	E11416 Primer. 9/2
c 559	10.4	45.2	24	6	AR174006	AR174006 Sequence	c 632	10.4	45.2	33	6	A45492	A45492 Sequence 21
c 560	10.4	45.2	24	6	AX038337	AX038337 Sequence	c 633	10.4	45.2	33	6	AR004355	AR004355 Sequence
c 561	10.4	45.2	24	6	AX111721	AX111721 Sequence	c 634	10.4	45.2	33	6	AR004396	AR004396 Sequence
c 562	10.4	45.2	24	6	AX111724	AX111724 Sequence	c 635	10.4	45.2	33	6	AR064935	AR064935 Sequence
c 563	10.4	45.2	24	6	AX289430	AX289430 Sequence	c 636	10.4	45.2	33	6	AR097146	AR097146 Sequence
c 564	10.4	45.2	24	6	AX290052	AX290052 Sequence	c 637	10.4	45.2	33	6	AR097188	AR097188 Sequence
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c 566	10.4	45.2	24	6	E44016	E44016 Novel prote	c 639	10.4	45.2	33	6	AR130686	AR130686 Sequence
c 567	10.4	45.2	24	6	E59313	E59313 Method of r	c 640	10.4	45.2	33	6	AR171993	AR171993 Sequence
c 568	10.4	45.2	25	6	A87194	A87194 Sequence 5	c 641	10.4	45.2	33	6	AR172035	AR172035 Sequence
c 569	10.4	45.2	25	6	AX038338	AX038338 Sequence	c 642	10.4	45.2	33	6	BD006668	BD006668 Transport
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c 573	10.4	45.2	26	6	AR090495	AR090495 Sequence	c 646	10.4	45.2	34	6	AR032330	AR032330 Sequence
c 574	10.4	45.2	26	6	AR105759	AR105759 Sequence	c 647	10.4	45.2	34	6	AR085289	AR085289 Sequence
c 575	10.4	45.2	26	6	I14114	I14114 Sequence 28	c 648	10.4	45.2	34	6	AR095274	AR095274 Sequence
c 576	10.4	45.2	26	6	I22158	I22158 Sequence 17	c 649	10.4	45.2	34	6	AR153421	AR153421 Sequence
c 577	10.4	45.2	27	6	A02823	A02823 Artificial	c 650	10.4	45.2	34	6	AR178094	AR178094 Sequence
c 578	10.4	45.2	27	6	A21825	A21825 Polynucleot	c 651	10.4	45.2	34	6	AX085551	AX085551 Sequence
c 579	10.4	45.2	27	6	A22669	A22669 Oligonucleo	c 652	10.4	45.2	34	6	AX247553	AX247553 Sequence
c 580	10.4	45.2	27	6	AX099274	AX099274 Sequence	c 653	10.4	45.2	34	6	I17720	I17720 Sequence 24
c 581	10.4	45.2	27	6	AX099275	AX099275 Sequence	c 654	10.4	45.2	34	6	I28968	I28968 Sequence 17
c 582	10.4	45.2	27	6	AX191218	AX191218 Sequence	c 655	10.4	45.2	34	6	I38632	I38632 Sequence 24
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804	10.2	44.3	20	6	IL2671	IL2671 Sequence 81	c 877	10.2	44.3	31	6	AR019512	AR019512 Sequence
805	10.2	44.3	20	6	I40125	I40125 Sequence 7	c 878	10.2	44.3	31	6	AR035764	AR035764 Sequence
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c 807	10.2	44.3	21	6	AR102141	AR102141 Sequence	c 880	10.2	44.3	31	6	AR118764	AR118764 Sequence
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c 809	10.2	44.3	21	6	AR103185	AR103185 Sequence	c 882	10.2	44.3	31	6	AR248580	AR248580 Sequence
c 810	10.2	44.3	21	6	AX096100	AX096100 Sequence	c 883	10.2	44.3	31	6	AX249562	AX249562 Sequence
c 811	10.2	44.3	21	6	AX338686	AX338686 Sequence	c 884	10.2	44.3	31	6	I06396	I06396 Sequence 16
c 812	10.2	44.3	21	6	I81264	I81264 Sequence 15	c 885	10.2	44.3	31	6	I32171	I32171 Sequence 46
813	10.2	44.3	21	6	AR090575	AR090575 Sequence	c 886	10.2	44.3	31	6	I34262	I34262 Sequence 46
814	10.2	44.3	24	6	AR136099	AR136099 Sequence	c 887	10.2	44.3	31	6	I82467	I82467 Sequence 46
815	10.2	44.3	24	6	AX038254	AX038254 Sequence	c 888	10.2	44.3	32	6	AR003515	AR003515 Sequence
c 816	10.2	44.3	24	6	AX288818	AX288818 Sequence	c 889	10.2	44.3	32	6	AR070736	AR070736 Sequence
817	10.2	44.3	24	6	AX290367	AX290367 Sequence	c 890	10.2	44.3	32	6	AR174849	AR174849 Sequence
c 818	10.2	44.3	24	6	AX291184	AX291184 Sequence	c 891	10.2	44.3	32	6	AX181033	AX181033 Sequence
819	10.2	44.3	24	6	AX291959	AX291959 Sequence	c 892	10.2	44.3	32	6	I62411	I62411 Sequence 17
820	10.2	44.3	24	6	AX292034	AX292034 Sequence	c 893	10.2	44.3	32	6	A69018	A69018 Sequence 6
c 821	10.2	44.3	24	6	AX292435	AX292435 Sequence	c 894	10.2	44.3	33	6	A95952	A95952 Sequence 6
c 822	10.2	44.3	24	6	I15804	I15804 PCR primer.	c 895	10.2	44.3	33	6	AR021437	AR021437 Sequence
c 823	10.2	44.3	24	6	I44524	I44524 Sequence 37	c 896	10.2	44.3	33	6	AR035445	AR035445 Sequence
824	10.2	44.3	25	6	AR109594	AR109594 Sequence	c 897	10.2	44.3	33	6	AR042999	AR042999 Sequence
825	10.2	44.3	25	6	AR150642	AR150642 Sequence	c 898	10.2	44.3	33	6	AR085058	AR085058 Sequence
c 826	10.2	44.3	25	6	AX297662	AX297662 Sequence	c 899	10.2	44.3	33	6	AR157898	AR157898 Sequence
827	10.2	44.3	25	6	AX349887	AX349887 Sequence	c 900	10.2	44.3	33	6	AR161332	AR161332 Sequence
828	10.2	44.3	25	6	E12465	E12465 PCR primer	c 901	10.2	44.3	33	6	AX250491	AX250491 Sequence
829	10.2	44.3	25	6	E12659	E12659 Primer. 6/1	c 902	10.2	44.3	33	6	AX343773	AX343773 Sequence
830	10.2	44.3	25	6	E14220	E14220 Primer. 7/1	c 903	10.2	44.3	33	6	AX280415	AX280415 Sequence
831	10.2	44.3	25	6	E16191	E16191 Primer. 7/1	c 904	10.2	44.3	33	6	BD001835	BD001835 Trimer ch
832	10.2	44.3	25	6	E27217	E27217 Novel physl	c 905	10.2	44.3	33	6	BD006095	BD006095 Feline po
833	10.2	44.3	25	6	E28275	E28275 Utilization	c 906	10.2	44.3	33	6	I62990	I62990 Sequence 11
834	10.2	44.3	25	6	E37241	E37241 Novel physl	c 907	10.2	44.3	33	6	I88743	I88743 Sequence 11
c 835	10.2	44.3	25	6	I68649	I68649 Sequence 14	c 908	10.2	44.3	34	6	A28098	A28098 Human GABA
836	10.2	44.3	25	23	HUMMOFRB	L32785 Homo sapien	c 909	10.2	44.3	34	6	A39293	A39293 Sequence 18
837	10.2	44.3	25	23	E11747	E11747 Primer for	c 910	10.2	44.3	34	6	AR028333	AR028333 Sequence
838	10.2	44.3	26	6	AR003516	AR003516 Sequence	c 911	10.2	44.3	34	6	AR148589	AR148589 Sequence
839	10.2	44.3	26	6	AR070748	AR070748 Sequence	c 912	10.2	44.3	34	6	AR148590	AR148590 Sequence
840	10.2	44.3	26	6	AX136874	AX136874 Sequence	c 913	10.2	44.3	34	6	AX286286	AX286286 Sequence
841	10.2	44.3	26	6	IL17673	IL17673 Sequence 20	c 914	10.2	44.3	34	6	I24931	I24931 Sequence 3
842	10.2	44.3	26	6	I62423	I62423 Sequence 29	c 915	10.2	44.3	34	6	I88874	I88874 Sequence 8
c 843	10.2	44.3	27	6	A76892	A76892 Sequence 24	c 916	10.2	44.3	35	6	AX151753	AX151753 Sequence
844	10.2	44.3	27	6	AR073724	AR073724 Sequence	c 917	10.2	44.3	36	6	AR064311	AR064311 Sequence
c 845	10.2	44.3	27	6	AR143859	AR143859 Sequence	c 918	10.2	44.3	36	6	AR137779	AR137779 Sequence
846	10.2	44.3	27	6	AX020800	AX020800 Sequence	c 919	10.2	44.3	36	6	AR142180	AR142180 Sequence
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c 853	10.2	44.3	27	6	E35726	E35726 Toxoplasma	c 926	10.2	44.3	37	6	AR003506	AR003506 Sequence
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c 856	10.2	44.3	28	6	AR035843	AR035843 Sequence	c 929	10.2	44.3	37	6	AX080997	AX080997 Sequence
c 857	10.2	44.3	28	6	AR035844	AR035844 Sequence	c 930	10.2	44.3	37	6	AX093425	AX093425 Sequence
c 858	10.2	44.3	28	6	AX203630	AX203630 Sequence	c 931	10.2	44.3	37	6	I16164	I16164 Sequence 15
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c 860	10.2	44.3	29	6	AR1006182	AR1006182 Sequence	c 933	10.2	44.3	38	6	AR004623	AR004623 Sequence
c 861	10.2	44.3	29	6	AX100907	AX100907 Sequence	c 934	10.2	44.3	38	6	AR064005	AR064005 Sequence
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c 863	10.2	44.3	29	6	AX203634	AX203634 Sequence	c 936	10.2	44.3	38	6	AX174845	AX174845 Sequence
c 864	10.2	44.3	29	6	AX254750	AX254750 Sequence	c 937	10.2	44.3	38	6	BD007241	BD007241 Novel flt
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c 866	10.2	44.3	30	6	A50095	A50095 Sequence 47	c 939	10.2	44.3	38	6	E55295	E55295 Novel metal
c 867	10.2	44.3	30	6	AR083374	AR083374 Sequence	c 940	10.2	44.3	38	6	I26932	I26932 Sequence 2
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870	10.2	44.3	30	6	AR092902	AR092902 Sequence	c 943	10.2	44.3	38	9	HUMTCVPD1DX	L32473 Human (clon
871	10.2	44.3	30	6	AR129814	AR129814 Sequence	c 944	10.2	44.3	39	4	BTA235258	Bos tauru
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c 875	10.2	44.3	31	6	A50061	A50061 Sequence 13	c 948	10.2	44.3	39	6	L39510	Homo sapien
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950 10.2 44.3 40 6 AR086366 Sequence
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970 10.2 44.3 42 6 BD006877 Oligonucle
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987 10.2 44.3 44 6 AR112979 Sequence
988 10.2 44.3 45 6 A05114
989 10.2 44.3 45 6 AR035459 Sequence
990 10.2 44.3 45 6 AR043538 Sequence
991 10.2 44.3 45 6 AR103991 Sequence
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995 10.2 44.3 45 9 S80667
996 10.2 44.3 46 6 AR087647 Sequence
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ALIGNMENTS

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RESULT 1
AX009578
LOCUS AX009578 23 bp DNA linear PAT 06-SEP-2000
DEFINITION Sequence 3 from Patent WO9961607.
ACCESSION AX009578
VERSION AX009578.1 GI:9996816
KEYWORDS
SOURCE synthetic construct.
ORGANISM synthetic construct
REFERENCE 1 (bases 1 to 23)
AUTHORS Deinert,I., Boehle,A., Gerdes,J. and Flad,H.D.
TITLE Antisense oligonucleotides for treating proliferating cells
JOURNAL Patent: WO 9961607-A 3 02-DEC-1999;
DEINERT IRINA (DE); BOEHLE ANDREAS (DE); GERDES JOHANNES (DE); FLAD
HANS DIETER (DE); FORSCHUNGSZENTRUM BORSTEL ZENT (DE)
FEATURES
Location/Qualifiers
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Qy 1 accaggcgctcgtgggccacat 23
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RESULT 2
AR044526
LOCUS AR044526 23 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 66 from patent US 5817495.
ACCESSION AR044526
VERSION AR044526.1 GI:5965991
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 23)
AUTHORS Pedersen,A.Hjelholt., Vind,J., Svendsen,A., Cherry,J.R., Lamsa,M.,
Schneider,P. and Jensen,B.Rostgaard.
TITLE H.sub.2 O.sub.2 -stable peroxidase variants
JOURNAL H.sub.2 O.sub.2 -stable peroxidase variants
FEATURES
Location/Qualifiers
SOURCE 1..23
BASE COUNT 6 a 7 c 6 g 4 t
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Query Match 63.5%; Score 14.6; DB 6; Length 23;
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RESULT 3
AX350362
LOCUS AX350362 37 bp DNA linear PAT 06-FEB-2002
DEFINITION Sequence 18 from Patent WO0202765.
ACCESSION AX350362
VERSION AX350362.1 GI:18616024
KEYWORDS
SOURCE synthetic construct.
ORGANISM synthetic construct
REFERENCE 1 (sites)
AUTHORS Ribault,S., Neuville,P. and Mehtali,M.
TITLE Chimeric promoters for controlling expression in smooth muscle
JOURNAL Patent: WO 0202765-A 18 10-JAN-2002;
TRANSGENE S.A. (FR)
FEATURES
Location/Qualifiers
SOURCE 1..37
ORGANISM synthetic construct
REFERENCE 1 (bases 1 to 23)
AUTHORS Ribault,S., Neuville,P. and Mehtali,M.
TITLE Chimeric promoters for controlling expression in smooth muscle
JOURNAL Patent: WO 0202765-A 18 10-JAN-2002;
TRANSGENE S.A. (FR)
FEATURES
Location/Qualifiers
SOURCE 1..37
BASE COUNT 9 a 10 c 12 g 6 t
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Best Local Similarity 84.2%; Pred. No. 1.8e+04;
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RESULT 4
I25110/c I25110 34 bp DNA linear PAT 07-OCT-1996
LOCUS DEFINITION Sequence 16 from patent US 5547868.
ACCESSION I25110
VERSION I25110.1 GI:1604980

KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 34)
AUTHORS Miller,W.L., Harikrishna,J.A. and Black,S.M.
TITLE Cholesterol disposal fusion enzymes
JOURNAL Patent: US 5547868-A 16 20-AUG-1996;
FEATURES Location/Qualifiers
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BASE COUNT 4 a 10 c 16 g 4 t
ORIGIN

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Best Local Similarity 88.2%; Pred. No. 2.9e+04;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 6 gcgtctcgtggccca 22
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RESULT 5
LOCUS AR058898/c AR058898 20 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 4 from patent US 5837836.
ACCESSION AR058898
VERSION AR058898.1 GI:5984475

KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 20)
AUTHORS Friderici,K., Jones,M.Z., Chen,H. and Cavanagh,K.T.
TITLE Bovine beta-mannosidase nucleic acid sequence
JOURNAL Patent: US 5837836-A 4 17-NOV-1998;
FEATURES Location/Qualifiers
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/organism="unknown"

BASE COUNT 7 a 5 c 5 g 3 t
ORIGIN

Query Match 59.1%; Score 13.6; DB 6; Length 20;
Best Local Similarity 80.0%; Pred. No. 3.6e+04;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 4 aggcgtctcgtggccacat 23
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Db 20 AGGTGCTCGTTAGCCACTT 1

RESULT 6
I36259/c I36259 20 bp DNA linear PAT 13-MAY-1997
LOCUS DEFINITION Sequence 4 from patent US 5605797.

ACCESSION I36259
VERSION I36259.1 GI:2086772
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 20)
AUTHORS Friderici,K., Jones,M.Z., Chen,H. and Cavanagh,K.T.
TITLE Bovine beta-mannosidase gene and methods of use
JOURNAL Patent: US 5605797-A 4 25-FEB-1997;
FEATURES Location/Qualifiers
1..20
/organism="unknown"

BASE COUNT 7 a 5 c 5 g 3 t
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Query Match 59.1%; Score 13.6; DB 6; Length 20;
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Db 20 AGGTGCTCGTTAGCCACTT 1

RESULT 7
A27934 A27934 45 bp DNA linear PAT 27-JUN-1995
LOCUS DEFINITION Reshaped VI CDR-2 primer.
ACCESSION A27934
VERSION A27934.1 GI:1248522

KEYWORDS
SOURCE Synthetic construct.
ORGANISM Synthetic construct.
REFERENCE 1 (bases 1 to 45)
AUTHORS HUMANIZED AND CHIMERIC MONOCLONAL ANTIBODIES
JOURNAL Patent: WO 9215683-A 23 17-SEP-1992;
FEATURES Location/Qualifiers
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/organism="synthetic construct"

BASE COUNT 9 a 15 c 10 g 11 t
ORIGIN

Query Match 59.1%; Score 13.6; DB 6; Length 45;
Best Local Similarity 80.0%; Pred. No. 3.6e+04;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 accaggcgtctcgtggccca 20
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Db 23 ACCTGCTCTGCTGTCCTG 42

RESULT 8
AR050879 AR050879 45 bp DNA linear PAT 29-SEP-1999
LOCUS DEFINITION Sequence 33 from patent US 5830470.
ACCESSION AR050879
VERSION AR050879.1 GI:5974243

KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 45)
AUTHORS Nakamura,K., Koike,M., Shitara,K., Hanai,N., Kuwana,Y. and Hasegawa,M.
TITLE Humanized antibodies to ganglioside GM.sub.2
JOURNAL Patent: US 5830470-A 33 03-NOV-1998;
FEATURES Location/Qualifiers

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Best Local Similarity 80.0%; Pred. No. 3.6e+04;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 accaggcgtctcgtggccca 20
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Db 25 ACCTGGCTTCTGGTGTGCCA 44

RESULT 9
LOCUS I26287 45 bp DNA linear PAT 07-OCT-1996
DEFINITION Sequence 36 from patent US 5558864.
ACCESSION I26287
VERSION I26287.1 GI:1606157
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 45)
AUTHORS Bendig,M.M., Kettleborough,C.A. and Saldanha,J.
TITLE Humanized and chimeric anti-epidermal growth factor receptor
monoclonal antibodies
JOURNAL Patent: US 5558864-A 36 24-SEP-1996;
FEATURES Location/Qualifiers
source 1. .45
/organism="unknown"
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ORIGIN

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Best Local Similarity 80.0%; Pred. No. 3.6e+04;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 accaggcgtctcgtggccca 20
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Db 23 ACCTGGCTTCTGGTGTGCCA 42

RESULT 10
I51659/c
LOCUS I51659 45 bp DNA linear PAT 07-OCT-1997
DEFINITION Sequence 6 from patent US 5645817.
ACCESSION I51659
VERSION I51659.1 GI:2472860
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 45)
AUTHORS Seemann,G. and Bosslet,K.
TITLE Granulocyte-binding antibody constructs, their preparation and use
JOURNAL Patent: US 5645817-A 6 08-JUL-1997;
FEATURES Location/Qualifiers
source 1. .45
/organism="unknown"
BASE COUNT 11 a 10 c 16 g 8 t
ORIGIN

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Best Local Similarity 80.0%; Pred. No. 3.6e+04;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 accaggcgtctcgtggccca 20
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Db 23 ACCTGGCTTCTGGTGTGCCA 44
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Db 23 ACCTGGCTTCTGGTGTGCCA 4

RESULT 11
LOCUS A57109 42 bp DNA linear PAT 03-MAR-1998
DEFINITION Sequence 5 from Patent WO9630507.
ACCESSION A57109
VERSION A57109.1 GI:3713089
KEYWORDS
SOURCE unidentified.
ORGANISM unclassified.
REFERENCE 1 (bases 1 to 42)
AUTHORS Goding,C.R., White,M., Yavuzer,B.U. and Hurd,D.
TITLE VECTORS FOR DIFFERENTIAL EXPRESSION
JOURNAL Patent: WO 9630507-A 5 03-OCT-1996;
AMERSHAM INT PLC (GB)
FEATURES Location/Qualifiers
source 1. .42
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BASE COUNT 12 a 10 c 11 g 9 t
ORIGIN

Query Match 58.3%; Score 13.4; DB 6; Length 42;
Best Local Similarity 73.9%; Pred. No. 4.5e+04;
Matches 17; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 accaggcgtctcgtggccacat 23
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Db 9 AGCATGCATCTAGAGGGCCGCAT 31

RESULT 12
AX159478
LOCUS AX159478 50 bp DNA linear PAT 22-JUN-2001
DEFINITION Sequence 2806 from Patent WO0140521.
ACCESSION AX159478
VERSION AX159478.1 GI:14540809
KEYWORDS human.
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 50)
AUTHORS Shimkets,R.A. and Leach,M.
TITLE Nucleic acids containing single nucleotide polymorphisms and
methods of use thereof
JOURNAL Patent: WO 0140521-A 2806 07-JUN-2001;
Curagen Corporation (US)
FEATURES Location/Qualifiers
source 1. .50
/organism="Homo sapiens"
/db_xref="taxon:9606"
misc_feature 25. .26
/notes="Nucleotide deleted between bases 25 and 26
Accession number cg42500135"
misc_feature 26
/notes="2 of 2 allelic variants (2805 is other entry)"
BASE COUNT 5 a 13 c 23 g 9 t
ORIGIN

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Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 3 caggcgtctcgtggccca 20
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Query Match          56.5%; Score 13; DB 6; Length 29;
Best Local Similarity 76.2%; Pred. No. 7.2e+04;
Matches 16; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
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GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: August 17, 2002, 22:20:00 ; Search time 209.43 Seconds
(without alignments)
188.555 Million cell updates/sec

Title: US-09-700-906A-3

Perfect score: 23

Sequence: 1 accaggcgtctcgtggccacat 23

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1736436 seqs, 858457221 residues

Total number of hits satisfying chosen parameters: 1905168

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	ID	Description
1	23	100.0	23 21	Human cell cycle p
c 2	23	100.0	23 21	Human cell cycle p
3	14.6	63.5	48 15	Human beta-glucuro
c 4	14.2	61.7	30 20	PCR primer of the
5	14	60.9	50 22	Human SNP oligonuc
c 6	14	60.9	50 22	Human SNP oligonuc
c 7	13.8	60.0	34 16	Adrenodoxin-reduct
c 8	13.8	60.0	47 21	Human map-related
9	13.8	60.0	48 15	E.coli beta-glucur

10	13.8	60.0	48	15	AAQ78241	Primer for amplify
c 11	13.6	59.1	20	18	AAQ62433	Bovine beta-mannos
c 12	13.6	59.1	20	20	AAV64130	Bovine beta-mannos
13	13.6	59.1	45	15	AAQ63451	REI human Ab L cha
14	13.6	59.1	45	20	AAQ99493	Synthetic DNA for
c 15	13.4	58.3	27	19	AAV32874	Human Borna disease
c 16	13.4	58.3	42	17	AAQ39606	CYC terminator pri
17	13.2	57.4	50	22	AAI75865	Human silent SNP c
c 18	13	56.5	25	22	AAI75369	CHO MEK gene PCR p
c 19	13	56.5	41	22	AAI65184	Growth hormone fam
c 20	13	56.5	41	22	AAI65185	Growth hormone fam
21	13	56.5	42	21	AAA65068	Exemplary DNA #6 e
22	13	56.5	42	21	AAA65069	Exemplary DNA #7 e
23	13	56.5	50	22	AAI30289	Human SNP oligonuc
24	12.8	55.7	28	24	ABA03536	Relaxin/IGF/insuli
c 25	12.8	55.7	31	22	AAI65697	M tuberculosis lys
c 26	12.8	55.7	47	21	AAZ66679	Human map-related
c 27	12.6	54.8	21	19	AAZ25868	Human polymorphic
c 28	12.6	54.8	27	19	AAV66554	Oligonucleotide 10
c 29	12.6	54.8	27	19	AAV38490	Human beta-globin
30	12.6	54.8	27	21	AAZ40651	V. cholerae tbyA q
31	12.6	54.8	28	18	AAI88886	Primer CTN2 for Fa
32	12.6	54.8	28	19	AAV70124	Human Fas antigen
33	12.6	54.8	28	21	AAA72113	Mouse IL-3 recepto
c 34	12.6	54.8	28	21	AAA11551	Human Fas antigen
c 35	12.6	54.8	34	19	AAV08045	Primer for coding
c 36	12.6	54.8	41	19	AAV26397	Humanised antibody
c 37	12.6	54.8	41	19	AAV21675	Humanised antibody
38	12.6	54.8	50	22	AAI75839	Human silent SNP c
39	12.4	53.9	25	22	AAI10689	Strand 1 of DX (do
40	12.4	53.9	29	22	AAI57490	Camel binder IDBOV
41	12.4	53.9	29	22	AAI57492	MHC class I allele
c 42	12.4	53.9	31	16	AAQ85848	MHC CW3 amplifcat
c 43	12.4	53.9	31	16	AAQ85778	MHC CW3 amplifcat
c 44	12.4	53.9	31	16	AAQ85742	MHC CW3 cDNA nts 1
45	12.4	53.9	37	20	AAI90420	Human p53 gene pri
46	12.4	53.9	40	21	AAQ63106	Shiga-like toxin 1
47	12.4	53.9	41	21	AAQ63105	Shiga-like toxin 1
48	12.4	53.9	42	21	AAQ63104	Shiga-like toxin 1
49	12.4	53.9	44	20	AAI87548	Erwinia herbicola
50	12.4	53.9	44	20	AAI62586	Oligonucleotide Cr
51	12.4	53.9	50	22	AAI34518	Human SNP oligonuc
52	12.4	53.9	50	22	AAI34573	Human SNP oligonuc
c 53	12.4	53.9	50	22	AAI09047	Human oligonucleot
54	12.2	53.0	20	24	AAI95090	Capture oligonucle
c 55	12.2	53.0	23	24	AAI22420	Human collagen COL
56	12.2	53.0	24	24	AAI86750	Capture oligonucle
c 57	12.2	53.0	24	24	AAI86751	Capture oligonucle
c 58	12.2	53.0	26	21	AAI54898	Neisseria species
59	12.2	53.0	31	18	AAI43374	SAR element PCR pr
60	12.2	53.0	38	20	AAI56345	Neisseria gonorrhoe
c 61	12.2	53.0	46	20	AAI26503	WO 990191 SeqID #
62	12	52.2	20	20	AAI08885	Human PECAM-1 anti
63	12	52.2	22	19	AAI62369	A. utahensis ECB d
64	12	52.2	22	19	AAI62031	A. utahensis ECB d
65	12	52.2	24	13	AAQ30865	c-kit mRNA antisen
66	12	52.2	24	13	AAQ37317	Antisense oligonuc
67	12	52.2	25	13	AAQ30864	c-kit mRNA antisen
68	12	52.2	26	13	AAQ30863	c-kit mRNA antisen
c 69	12	52.2	26	13	AAQ37315	Antisense oligonuc
c 70	12	52.2	29	21	AAI04005	Polymorphic fragme
c 71	12	52.2	31	22	AAI29754	Human single nucle
72	12	52.2	33	24	AAI99823	Human short chain
73	12	52.2	34	22	AAI26266	B. megaterium BM-3
c 74	12	52.2	34	22	AAI26267	B. megaterium BM-3
75	12	52.2	37	16	AAQ98445	Antisense probe DM
76	12	52.2	37	20	AAI24984	Oligonucleotide DM
77	12	52.2	40	13	AAQ30862	c-kit mRNA antisen
78	12	52.2	40	21	AAI37327	Human c-kit fragme
79	12	52.2	42	21	AAI65063	Exemplary DNA #1
80	12	52.2	42	21	AAI65071	Exemplary DNA #9 e
c 81	12	52.2	47	18	AAI48616	Catalytic DNA, met
82	12	52.2	47	21	AAI67343	Human map-related

c 83	11.8	51.3	20	22	AAK94980	Human cDNA clone-s	156	11.6	50.4	41	19	AAV41677	Glucose-inducible
c 84	11.8	51.3	22	24	AAD24620	Trichoderma reesei	157	11.6	50.4	43	12	AAQ12253	HIV-1 LTR mutation
c 85	11.8	51.3	24	21	AAA47675	RACE oligo d(T) an	158	11.6	50.4	43	22	AAQ09082	Human oligonucleot
c 86	11.8	51.3	24	21	AAA43425	Linker variant pol	159	11.6	50.4	48	17	AAT06971	DNA encoding GW-CS
c 87	11.8	51.3	24	21	AAA45931	Linker variant pol	160	11.6	50.4	50	18	AAT78670	Construction oligo
c 88	11.8	51.3	24	24	AAS62843	DNA linker #5 for	161	11.6	50.4	50	22	AAL30342	Human SNP oligonuc
c 89	11.8	51.3	26	18	AAT60609	Human cysteine pro	162	11.4	49.6	13	23	ABC51158	Oligonucleotide SE
c 90	11.8	51.3	29	22	AAD18771	Primer Y2H-MCS2, t	c 163	11.4	49.6	13	23	ABC51159	Oligonucleotide SE
c 91	11.8	51.3	31	19	AAH10524	Human ITAK cDNA li	164	11.4	49.6	13	23	ABC51180	Oligonucleotide SE
c 92	11.8	51.3	31	22	AAH47094	B. napus cold indu	c 165	11.4	49.6	13	23	ABC51181	Oligonucleotide SE
c 93	11.8	51.3	31	22	AAI29665	Human single nucle	c 166	11.4	49.6	17	20	AAH44577	Human mACHR-6 anti
c 94	11.8	51.3	31	22	AAI30503	Human single nucle	c 167	11.4	49.6	17	20	AAH44577	Human mACHR-6 anti
c 95	11.8	51.3	32	20	AAI19726	Human AIM-1 PCR pr	c 168	11.4	49.6	17	20	AAH44577	Human mACHR-6 anti
c 96	11.8	51.3	32	20	AAH24148	Human E2F-1 promot	169	11.4	49.6	19	21	AAH83539	Cdk-we-hu ribozyme
c 97	11.8	51.3	39	19	AAV62466	Oligo-dT-anchor pr	170	11.4	49.6	19	22	AAH58701	Cdk-we-hu ribozyme
c 98	11.8	51.3	39	19	AAV60309	Oligo-dT anchor pr	171	11.4	49.6	21	22	AAH58701	Human gene single
c 99	11.8	51.3	39	20	AAZ32554	Anchor tailed prim	172	11.4	49.6	21	22	AAH58701	PCR anchor primer.
c 100	11.8	51.3	39	20	AAZ32559	Anchor tailed prim	173	11.4	49.6	22	19	AAV60310	PCR anchor primer.
c 101	11.8	51.3	39	20	AAH81830	PCR primer used to	174	11.4	49.6	22	20	AAZ32556	Anchor primer, for
c 102	11.8	51.3	39	20	AAH81836	PCR primer used to	175	11.4	49.6	22	20	AAZ32561	Anchor primer, for
c 103	11.8	51.3	39	21	AAZ50155	Oligo dT-anchor pr	176	11.4	49.6	22	20	AAZ32566	Anchor primer, for
c 104	11.8	51.3	39	22	AAH48707	T. thermophila tri	177	11.4	49.6	22	20	AAZ36784	PCR primer for hum
c 105	11.8	51.3	39	22	AAH48707	T. thermophila tri	178	11.4	49.6	22	20	AAZ36784	PCR primer AP used
c 106	11.8	51.3	39	22	AAH48707	T. thermophila tri	179	11.4	49.6	22	21	AAZ36784	PCR primer AP used
c 107	11.8	51.3	39	22	AAH48707	T. thermophila tri	180	11.4	49.6	22	21	AAZ36784	PCR primer AP used
c 108	11.8	51.3	39	22	AAH48707	T. thermophila tri	181	11.4	49.6	22	21	AAZ36784	PCR primer AP used
c 109	11.8	51.3	40	22	AAH48707	T. thermophila tri	182	11.4	49.6	22	22	AAH42284	5' sense anchor PC
c 110	11.8	51.3	40	22	AAH48707	T. thermophila tri	183	11.4	49.6	22	22	AAH42284	Primer used to amp
c 111	11.8	51.3	40	22	AAH48707	T. thermophila tri	184	11.4	49.6	22	22	AAH42284	Anchor primer, for
c 112	11.8	51.3	40	22	AAH48707	T. thermophila tri	185	11.4	49.6	22	22	AAH42284	Anchor primer, for
c 113	11.8	51.3	40	22	AAH48707	T. thermophila tri	186	11.4	49.6	22	22	AAH42284	Anchor primer, for
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c 126	11.6	50.4	42	20	AAH48707	T. thermophila tri	199	11.4	49.6	22	22	AAH42284	Anchor primer, for
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c 131	11.6	50.4	42	20	AAH48707	T. thermophila tri	204	11.4	49.6	22	22	AAH42284	Anchor primer, for
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c 133	11.6	50.4	42	20	AAH48707	T. thermophila tri	206	11.4	49.6	22	22	AAH42284	Anchor primer, for
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c 140	11.6	50.4	42	20	AAH48707	T. thermophila tri	213	11.4	49.6	22	22	AAH42284	Anchor primer, for
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c 143	11.6	50.4	42	20	AAH48707	T. thermophila tri	216	11.4	49.6	22	22	AAH42284	Anchor primer, for
c 144	11.6	50.4	42	20	AAH48707	T. thermophila tri	217	11.4	49.6	22	22	AAH42284	Anchor primer, for
c 145	11.6	50.4	42	20	AAH48707	T. thermophila tri	218	11.4	49.6	22	22	AAH42284	Anchor primer, for
c 146	11.6	50.4	42	20	AAH48707	T. thermophila tri	219	11.4	49.6	22	22	AAH42284	Anchor primer, for
c 147	11.6	50.4	42	20	AAH48707	T. thermophila tri	220	11.4	49.6	22	22	AAH42284	Anchor primer, for
c 148	11.6	50.4	42	20	AAH48707	T. thermophila tri	221	11.4	49.6	22	22	AAH42284	Anchor primer, for
c 149	11.6	50.4	42	20	AAH48707	T. thermophila tri	222	11.4	49.6	22	22	AAH42284	Anchor primer, for
c 150	11.6	50.4	42	20	AAH48707	T. thermophila tri	223	11.4	49.6	22	22	AAH42284	Anchor primer, for
c 151	11.6	50.4	42	20	AAH48707	T. thermophila tri	224	11.4	49.6	22	22	AAH42284	Anchor primer, for
c 152	11.6	50.4	42	20	AAH48707	T. thermophila tri	225	11.4	49.6	22	22	AAH42284	Anchor primer, for
c 153	11.6	50.4	42	20	AAH48707	T. thermophila tri	226	11.4	49.6	22	22	AAH42284	Anchor primer, for
c 154	11.6	50.4	42	20	AAH48707	T. thermophila tri	227	11.4	49.6	22	22	AAH42284	Anchor primer, for
c 155	11.6	50.4	42	20	AAH48707	T. thermophila tri	228	11.4	49.6	22	22	AAH42284	Anchor primer, for

c 229	11.4	49.6	36	21	AAA33319	Low adenosine anti	302	11.2	48.7	24	24	AB186364	Capture oligonucle
c 230	11.4	49.6	36	21	AAA335845	Permutin linked e	c 303	11.2	48.7	24	24	AB186365	Capture oligonucle
c 231	11.4	49.6	38	20	AAZ32559	Anchor tailed prim	c 304	11.2	48.7	24	24	AB192244	Capture oligonucle
c 232	11.4	49.6	38	20	AAZ32564	Anchor tailed prim	c 305	11.2	48.7	24	24	AB192245	Capture oligonucle
c 233	11.4	49.6	38	20	AAZ45535	Tumour-specific Ig	c 306	11.2	48.7	25	20	AAZ21480	Primer #1 for fusi
c 234	11.4	49.6	39	20	AAZ24492	CC49/218 SCA (sing	c 307	11.2	48.7	26	21	AAZ40042	PCR primer MO10BAC
c 235	11.4	49.6	40	21	AAZ96092	Polynucleotide seq	c 308	11.2	48.7	27	20	AAZ80155	Human beta-1,4-gal
c 236	11.4	49.6	41	21	AAA09067	Primer for human h	c 309	11.2	48.7	27	20	AAZ58602	Human cancer anti
c 237	11.4	49.6	41	22	AA170160	Human uroplakin Ia	c 310	11.2	48.7	27	21	AAZ53308	PCR primer hGT-6Sp
c 238	11.4	49.6	41	22	AAZ62364	PCR primer used to	c 311	11.2	48.7	28	21	AAZ58380	Rapamycin rapc gen
c 239	11.4	49.6	42	22	AAH91968	Human inflammatory	c 312	11.2	48.7	29	20	AAA19923	Integrin alpha 6 s
c 240	11.4	49.6	44	15	AAQ78507	Human GRP78 Noti-1	c 313	11.2	48.7	29	20	AAZ22170	Integrin subunit b
c 241	11.4	49.6	44	20	AAZ81811	Primer used to amp	c 314	11.2	48.7	29	21	AAZ22170	Hammerhead ribozym
c 242	11.4	49.6	45	13	AAQ27685	FGS2 RNA for an ep	c 315	11.2	48.7	29	21	AAZ03738	Hammerhead ribozym
c 243	11.4	49.6	45	13	AAQ27689	FGS2 RNA for an ep	c 316	11.2	48.7	29	21	AAZ03738	Hammerhead ribozym
c 244	11.4	49.6	45	22	AAZ19606	Mutagenic PCR prim	c 317	11.2	48.7	29	21	AAZ05847	Hammerhead ribozym
c 245	11.4	49.6	45	22	AAZ19607	Mutagenic_PCR prim	c 318	11.2	48.7	29	21	AAZ64524	Alphavirus synthes
c 246	11.4	49.6	45	22	AAH79093	Human insulin homo	c 319	11.2	48.7	29	21	AAZ23721	Oestrogen receptor
c 247	11.4	49.6	45	22	AAZ74532	Human MKK3 site-di	c 320	11.2	48.7	29	24	AAZ25115	Sindbis virus cDNA
c 248	11.4	49.6	45	22	AAZ74533	Human MKK3 site-di	c 321	11.2	48.7	30	20	AAZ58601	Human cancer anti
c 249	11.4	49.6	45	22	AAZ64157	Human MKK3 site-di	c 322	11.2	48.7	30	22	AAZ50135	Bacterial 23S/5S R
c 250	11.4	49.6	45	22	AAZ64158	Human MKK mutageni	c 323	11.2	48.7	30	22	AAZ50159	Bacterial 23S/5S R
c 251	11.4	49.6	47	21	AAZ67973	Human map-related	c 324	11.2	48.7	30	22	AAZ12945	Rainbow trout prep
c 252	11.4	49.6	47	21	AAZ69020	Human map-related	c 325	11.2	48.7	31	21	AAZ37405	PCR primer for hum
c 253	11.4	49.6	47	21	AAZ69080	Human map-related	c 326	11.2	48.7	31	22	AAZ31257	Human single nucle
c 254	11.4	49.6	48	12	AAQ14775	Rennin gene probe.	c 327	11.2	48.7	31	22	AAZ05705	Human DKG epsilon
c 255	11.4	49.6	48	13	AAQ27686	FGS2 RNA for an ep	c 328	11.2	48.7	36	19	AAZ66665	Anti-human Fas hum
c 256	11.4	49.6	48	13	AAQ27687	FGS2 RNA for an ep	c 329	11.2	48.7	36	20	AAZ78356	Humanised anti-Fas
c 257	11.4	49.6	48	13	AAQ27690	FGS2 RNA for an ep	c 330	11.2	48.7	38	20	AAZ82614	Oligonucleotide us
c 258	11.4	49.6	48	13	AAQ27691	FGS2 RNA for an ep	c 331	11.2	48.7	39	16	AAQ89094	Elastase DNA nucle
c 259	11.4	49.6	49	20	AAZ31116	RNA ligand to hTGF	c 332	11.2	48.7	39	16	AAQ89116	Elastase DNA nucle
c 260	11.4	49.6	50	22	AAZ29212	Human SNP oligonuc	c 333	11.2	48.7	40	14	AAQ41768	Myc EMSA probe pro
c 261	11.4	49.6	50	22	AAZ31279	Human SNP oligonuc	c 334	11.2	48.7	40	16	AAQ89110	Elastase DNA nucle
c 262	11.4	49.6	50	22	AAZ31354	Human SNP oligonuc	c 335	11.2	48.7	40	16	AAQ89115	Elastase DNA nucle
c 263	11.4	49.6	50	22	AAZ33627	Human SNP oligonuc	c 336	11.2	48.7	40	17	AAZ70617	Fibrin clot bindin
c 264	11.4	49.6	50	22	AAZ33628	Human SNP oligonuc	c 337	11.2	48.7	40	19	AAZ51064	Maize polymorphic
c 265	11.4	49.6	50	22	AAZ33628	Human SNP oligonuc	c 338	11.2	48.7	40	20	AAZ28137	PCR primer for hum
c 266	11.4	49.6	50	22	AAZ33628	Human silent SNP c	c 339	11.2	48.7	40	20	AAZ28139	PCR primer for hum
c 267	11.4	49.6	50	22	AAZ62796	Crosslinking probe	c 340	11.2	48.7	40	22	AAZ02686	Human follistatin-
c 268	11.2	48.7	16	18	AAZ68901	Human BCR exon 11	c 341	11.2	48.7	40	22	AAZ02688	Human follistatin-
c 269	11.2	48.7	17	20	AAZ02387	Integrin alpha 6 s	c 342	11.2	48.7	41	19	AAZ51059	Maize polymorphic
c 270	11.2	48.7	17	21	AAZ02620	Hammerhead ribozym	c 343	11.2	48.7	42	24	AAZ92491	Pseudomonas carbox
c 271	11.2	48.7	18	19	AAZ47173	Primer JCA276 used	c 344	11.2	48.7	42	24	ABA92492	Primer FKBP5fil-A
c 272	11.2	48.7	18	19	AAZ16023	PCR primer used to	c 345	11.2	48.7	43	19	AAZ05446	Yeast PCR primer F
c 273	11.2	48.7	18	21	AAZ63098	Human cellular pro	c 346	11.2	48.7	43	21	AAZ73401	Yeast PCR primer F
c 274	11.2	48.7	18	21	AAZ63100	Human cellular pro	c 347	11.2	48.7	43	21	AAZ55889	FKBP gene PCR prim
c 275	11.2	48.7	18	21	AAZ92557	Antisense oligonuc	c 348	11.2	48.7	43	21	AAZ13253	Adaptor #3 used in
c 276	11.2	48.7	18	21	AAZ92592	Antisense oligonuc	c 349	11.2	48.7	43	21	AAZ13254	Adaptor #4 used in
c 277	11.2	48.7	18	21	AAZ05267	PCR primer C-F use	c 350	11.2	48.7	43	21	AAZ29567	Human map-related
c 278	11.2	48.7	18	21	AAZ47029	Primer JCA276 for	c 351	11.2	48.7	47	21	AAZ66418	Human map-related
c 279	11.2	48.7	18	21	AAZ43282	Murine Sox2 gene P	c 352	11.2	48.7	47	21	AAZ69484	Human map-related
c 280	11.2	48.7	19	21	AAZ58670	Nucleotide sequenc	c 353	11.2	48.7	49	18	AAZ90308	Multiple cloning s
c 281	11.2	48.7	19	21	AAZ58672	Nucleotide sequenc	c 354	11.2	48.7	50	19	AAZ50040	Detection probe SE
c 282	11.2	48.7	19	21	AAZ58674	Nucleotide sequenc	c 355	11.2	48.7	50	22	AAZ27879	Human SNP oligonuc
c 283	11.2	48.7	19	21	AAZ58677	Nucleotide sequenc	c 356	11.2	48.7	50	22	AAZ28818	Human SNP oligonuc
c 284	11.2	48.7	19	21	AAZ58681	Nucleotide sequenc	c 357	11.2	48.7	50	22	AAZ29632	Human SNP oligonuc
c 285	11.2	48.7	19	21	AAZ58683	Nucleotide sequenc	c 358	11.2	48.7	50	22	AAZ29633	Human SNP oligonuc
c 286	11.2	48.7	20	20	AAZ31252	CCP5 gene inhibiti	c 359	11.2	48.7	50	22	AAZ31086	Human SNP oligonuc
c 287	11.2	48.7	20	21	AAZ63103	Human cellular pro	c 360	11.2	48.7	50	22	AAZ31087	Human SNP oligonuc
c 288	11.2	48.7	20	21	AAZ78367	Humanised anti-Fas	c 361	11	47.8	19	21	AAZ07654	Forward primer for
c 289	11.2	48.7	21	19	AAZ25900	Human polymorphic	c 362	11	47.8	20	16	AAZ95372	Primer B (Group 2,
c 290	11.2	48.7	21	20	AAZ15007	Plasmid pTNB110 co	c 363	11	47.8	20	20	AAZ38504	E. coli SecA antis
c 291	11.2	48.7	21	22	AAH00933	Trypanosomatidae d	c 364	11	47.8	20	22	AAZ45692	Human PARP-2 antis
c 292	11.2	48.7	22	18	AAZ88943	Bumper primer 3 fo	c 365	11	47.8	20	22	AAZ02948	Type-C natriuretic
c 293	11.2	48.7	23	20	AAZ34031	Human CDC28-#3 RNA	c 366	11	47.8	21	19	AAZ25869	Human polymorphic
c 294	11.2	48.7	23	20	AAZ00484	PCR primer B233 us	c 367	11	47.8	21	20	AAZ28198	Tumour antigen ant
c 295	11.2	48.7	23	20	AAZ78706	Human PRO615 rever	c 368	11	47.8	21	22	AAZ96054	Human gene single
c 296	11.2	48.7	23	21	AAZ87706	Human PRO615 rever	c 369	11	47.8	21	22	AAZ96693	Human gene single
c 297	11.2	48.7	23	21	AAZ58146	Primer nol4-3 used	c 370	11	47.8	22	19	AAZ09717	Human biallelic po
c 298	11.2	48.7	24	21	AAZ72580	PCR primer used to	c 371	11	47.8	22	19	AAZ21525	L-oncogene primer
c 299	11.2	48.7	24	21	AAZ12689	Capture oligonucle	c 372	11	47.8	23	13	AAZ30866	c-kit mRNA antisen
c 300	11.2	48.7	24	24	AB182978	Capture oligonucle	c 373	11	47.8	23	21	AAZ37318	Antisense oligonuc
c 301	11.2	48.7	24	24	AB182979	Capture oligonucle	c 374	11	47.8	24	19	AAZ40682	Primer 35S for her

375	11	47.8	26	16	AAQ89946	Listeria 16S rDNA	c 448	10.8	47.0	20	24	ABI96448	Capture oligonucle
376	11	47.8	26	18	AAQ22952	Human cathepsin Y	449	10.8	47.0	21	15	AAQ68443	Pseudomonas glutam
377	11	47.8	26	20	AAZ11424	Hypoxia responsive	450	10.8	47.0	21	15	AAQ26751	Human polymorphic
378	11	47.8	26	12	AAQ12009	Murine HRE DNA glu	451	10.8	47.0	21	22	AAF63369	Forward PCR primer
c 379	11	47.8	27	12	AAQ14971	Beta A/S globin ge	c 452	10.8	47.0	23	17	AAT10339	Anti-p. aeruginosa
380	11	47.8	27	14	AAQ35914	Human/monkey heavy	c 453	10.8	47.0	23	24	ABA04439	Human P1009 PCR p
381	11	47.8	27	15	AAQ56634	PCR primer for mou	454	10.8	47.0	24	14	AAQ46694	Beta-actin primer
382	11	47.8	27	18	AAT95133	Human or monkey Ig	455	10.8	47.0	24	14	AAQ47685	Beta-actin PCR pri
383	11	47.8	27	18	AAT92209	Monkey/human heavy	456	10.8	47.0	24	15	AAQ78130	Specific oligonucle
384	11	47.8	27	18	AAT62880	Human or monkey VH	c 457	10.8	47.0	24	17	AAT38351	G3PDH primer 2. S
385	11	47.8	27	19	AAV31393	Human or monkey he	c 458	10.8	47.0	24	18	AAT70485	Dystrophin reverse
386	11	47.8	27	19	AAV23271	Primer for Anti-CD	c 459	10.8	47.0	24	19	AAV46349	PCR primer for ser
387	11	47.8	27	19	AAV05661	Human/monkey Vh4 1	c 460	10.8	47.0	24	19	AAV41639	Nucleotide sequenc
c 388	11	47.8	27	21	AAV64489	Primer for triose	c 461	10.8	47.0	24	19	AAV16411	Primer used in pre
389	11	47.8	28	19	AAV66672	Mouse interleukin-	c 462	10.8	47.0	24	20	AAZ23114	G3PDH specific 3'
390	11	47.8	28	21	AAV78371	Fas antigen extrac	c 463	10.8	47.0	24	20	AAZ21558	3' PCR primer used
391	11	47.8	29	19	AAV42718	5' PCR primer used	c 464	10.8	47.0	24	20	AAZ21363	Prime HGA for G3PD
392	11	47.8	29	19	AAV23922	PCR primer for hum	c 465	10.8	47.0	24	20	AAZ01680	Human G3PDH PCR pr
c 393	11	47.8	29	22	AAF99441	Immunostimulatory	c 466	10.8	47.0	24	21	AAAG6957	PCR primer used to
394	11	47.8	30	19	AAV44993	15D3 antibody heav	c 467	10.8	47.0	24	21	AAAG2449	Human G3PDH antisense
c 395	11	47.8	30	20	AAZ10945	15D3 VH chain CDR3	c 468	10.8	47.0	24	21	AAA07402	PCR primer for gly
c 396	11	47.8	30	21	AAA49127	1265MAS primer use	c 469	10.8	47.0	24	21	AAZ58346	Human GAPDH specif
c 397	11	47.8	30	21	AAZ52110	Maize CGEVL32RB-ul	c 470	10.8	47.0	24	22	AAH22599	Human G3PDH specif
c 398	11	47.8	30	21	AAZ52116	Primer CGEVL32RB_u	c 471	10.8	47.0	24	22	AAH22460	GAPDH downstream a
399	11	47.8	32	19	AAV41678	Glucose-inducible	c 472	10.8	47.0	24	22	AAH22468	GAPDH downstream a
c 400	11	47.8	32	20	AAZ17755	Oligo #23 for ampl	c 473	10.8	47.0	24	22	AAH23652	Glyceraldehyde 3-p
c 401	11	47.8	32	21	AAA30780	Human GPR32 (K255A	c 474	10.8	47.0	24	22	AAF84204	G3PDH PCR primer.
c 402	11	47.8	32	21	AAA30781	Human GPR32 (K255A	c 475	10.8	47.0	24	22	AAF25091	PCR primer for M.
c 403	11	47.8	32	22	AAZ00349	PCR primer #3, use	c 476	10.8	47.0	24	22	AAAG8966	Human GAPDH cDNA r
c 404	11	47.8	33	13	AAQ31144	Probe 113 specific	c 477	10.8	47.0	24	24	ABA92499	Human G3PDH specif
c 405	11	47.8	33	14	AAQ46450	Hepatitis C virus	c 478	10.8	47.0	24	24	ABA05425	Human Hcscs-1 PCR
c 406	11	47.8	33	20	AAZ17754	Oligo #24 for ampl	c 479	10.8	47.0	24	24	ABA96191	Human G3PDH PCR pr
c 407	11	47.8	33	21	AAZ00551	Enhanced yellow fl	c 480	10.8	47.0	24	24	ABI82576	Capture oligonucle
c 408	11	47.8	33	22	AAZ05932	EVFP-C1 reverse PC	c 481	10.8	47.0	24	24	ABI82577	Capture oligonucle
c 409	11	47.8	34	18	AAV02499	Human tyrosine pho	c 482	10.8	47.0	24	24	ABI84870	Capture oligonucle
c 410	11	47.8	36	18	AAZ67301	Islet cell antigen	c 483	10.8	47.0	24	24	ABI84871	Capture oligonucle
c 411	11	47.8	36	22	AAZ16693	Cucumis melo Pii24	c 484	10.8	47.0	24	24	ABI84978	Capture oligonucle
c 412	11	47.8	36	22	AAZ55634	Primer for human e	c 485	10.8	47.0	24	24	ABI84979	Capture oligonucle
c 413	11	47.8	37	22	AAZ55105	PCR primer for M.	c 486	10.8	47.0	24	24	ABI87156	Capture oligonucle
c 414	11	47.8	39	24	ABA02832	Mycobacterium tube	c 487	10.8	47.0	24	24	ABI87157	Capture oligonucle
c 415	11	47.8	40	20	AAZ56318	Neisseria gonorrhoe	c 488	10.8	47.0	24	24	ABI88188	Capture oligonucle
c 416	11	47.8	40	21	AAZ96069	Polynucleotide seq	c 489	10.8	47.0	24	24	ABI88189	Capture oligonucle
c 417	11	47.8	40	22	AAZ18011	A. fumigatus codon	c 490	10.8	47.0	24	24	ABI89242	Capture oligonucle
c 418	11	47.8	40	22	AAZ166507	Rat SAPK interacti	c 491	10.8	47.0	24	24	ABI89243	Capture oligonucle
c 419	11	47.8	41	18	AAZ59260	Forward primer SIN	c 492	10.8	47.0	24	24	ABI89466	Capture oligonucle
c 420	11	47.8	41	20	AAZ58502	Forward primer SIN	c 493	10.8	47.0	24	24	ABI89467	Capture oligonucle
c 421	11	47.8	41	20	AAZ56317	Neisseria gonorrhoe	c 494	10.8	47.0	24	24	ABI89618	Capture oligonucle
c 422	11	47.8	42	21	AAZ87168	CaMV35S enhancer e	c 495	10.8	47.0	24	24	ABI89619	Capture oligonucle
c 423	11	47.8	45	19	AAZ26491	Human cytohesin-1	c 496	10.8	47.0	24	24	ABI91842	Capture oligonucle
c 424	11	47.8	45	19	AAZ26492	Human cytohesin-1	c 497	10.8	47.0	24	24	ABI91843	Capture oligonucle
c 425	11	47.8	45	20	AAZ02196	Human JEG62 PCR pr	c 498	10.8	47.0	24	24	ABI92772	Capture oligonucle
c 426	11	47.8	47	21	AAZ68926	Human map-related	c 499	10.8	47.0	24	24	ABI92773	Capture oligonucle
c 427	11	47.8	48	13	AAQ31373	IL-6R antibody pri	c 500	10.8	47.0	25	20	AAZ35971	Primer used to amp
c 428	11	47.8	48	15	AAQ56727	Sequence of oligo	c 501	10.8	47.0	25	21	AAZ87784	Rat SNORF36 recept
c 429	11	47.8	49	18	AAZ80483	Hepatoma AS-30D Ty	c 502	10.8	47.0	25	21	AAZ63752	Maize cytotype-spe
c 430	11	47.8	50	13	AAQ21752	HCV probe 42.LIA2C	c 503	10.8	47.0	25	21	AAZ62444	Human Akt-3 cDNA 3
c 431	11	47.8	50	21	AAZ77273	Human clone cq4398	c 504	10.8	47.0	26	19	AAV08044	Primer for coding
c 432	11	47.8	50	22	AAZ29962	Human SNP oligonuc	c 505	10.8	47.0	27	17	AAT15477	Primer for B7 open
c 433	11	47.8	50	22	AAZ131600	Human SNP oligonuc	c 506	10.8	47.0	27	19	AAV31778	Nucleotide sequenc
c 434	11	47.8	50	22	AAZ131601	Human SNP oligonuc	c 507	10.8	47.0	27	21	AAZ59847	HSV thymidine kina
c 435	11	47.8	50	22	AAZ33541	Human SNP oligonuc	c 508	10.8	47.0	28	19	AAZ67174	Oligonucleotide SE
c 436	10.8	47.0	16	20	AAZ57818	PCR primer for G.	c 509	10.8	47.0	28	19	AAZ61886	Plasmid pET-7 prom
c 437	10.8	47.0	17	20	AAZ57838	PCR primer for G.	c 510	10.8	47.0	29	15	AAZ69969	Degenerate primer
c 438	10.8	47.0	19	21	AAZ58280	cdk4 ribozyme bind	c 511	10.8	47.0	29	17	AAT39992	Primer back p1 for
c 439	10.8	47.0	19	22	AAZ57992	Celli-cycle depende	c 512	10.8	47.0	29	20	AAZ21830	Integrin subunit b
c 440	10.8	47.0	20	20	AAZ02322	PCR primer used to	c 513	10.8	47.0	29	21	AAZ04102	Polymorphic fragme
c 441	10.8	47.0	20	20	AAZ79780	PCR primer H14909	c 514	10.8	47.0	29	22	AAZ20324	S. pneumoniae murM
c 442	10.8	47.0	20	22	AAZ19437	Human delta-6-desa	c 515	10.8	47.0	29	24	AAZ17237	Upstream PCR prime
c 443	10.8	47.0	20	22	AAZ76129	Human tau gene 5'	c 516	10.8	47.0	30	15	AAQ66191	Primer for seven t
c 444	10.8	47.0	20	22	AAZ70526	Human DRD2 fragmen	c 517	10.8	47.0	30	15	AAQ66192	Primer for seven t
c 445	10.8	47.0	20	22	AAZ72518	G.ardea target seq	c 518	10.8	47.0	30	16	AAQ92607	Thermus thermophil
c 446	10.8	47.0	20	24	ABI93003	Capture oligonucle	c 519	10.8	47.0	30	18	AAZ58425	Apolipoprotein B g
c 447	10.8	47.0	20	24	ABI94897	Capture oligonucle	c 520	10.8	47.0	30	19	AAV18386	Human R20 seven tr

521	10.8	47.0	30	19	AAV18387	Human R20 seven tr	594	10.8	47.0	21	AAZ67019	Human map-related
522	10.8	47.0	30	20	AAx84889	PCR primer for hum	595	10.8	47.0	47	AAZ69480	Human map-related
523	10.8	47.0	30	20	AAV82536	Probe ApoB-1 used	c 596	10.8	47.0	48	AAV67171	pET-7 T7 promoter
524	10.8	47.0	30	21	AA91738	Human 7TM receptor	c 597	10.8	47.0	48	AAV61893	Plasmid pET-7 prom
525	10.8	47.0	30	21	AA91739	Human 7TM receptor	c 598	10.8	47.0	49	AA91016	Human chromosome 4
526	10.8	47.0	30	21	AAZ47329	PCR primer Sextole	599	10.8	47.0	49	AAZ94248	Plasmid pRAE-6 elo
527	10.8	47.0	30	22	AAH27627	Human histone deac	600	10.8	47.0	50	AAQ69629	Human metallothion
528	10.8	47.0	30	22	AAF32187	Human oestrogen re	601	10.8	47.0	50	AAQ64091	Human metallothion
529	10.8	47.0	30	22	AAF26871	3'-mer oligonucleo	602	10.8	47.0	50	AAV66666	Anti-human Fas hum
530	10.8	47.0	31	16	AAQ91866	Murine trkB tyrosi	603	10.8	47.0	50	AAV19377	PCR primer R370-98
531	10.8	47.0	31	20	AAx60079	3' untranslated re	604	10.8	47.0	50	AAV19378	PCR primer R371-98
532	10.8	47.0	31	21	AAV79204	Human genomic DNA	605	10.8	47.0	50	AAV17379	Test sequence from
533	10.8	47.0	31	22	AAI30877	Human single nucle	606	10.8	47.0	50	AAV78357	Humanised anti-Fas
534	10.8	47.0	31	23	AB197848	Non-endogenous hum	c 607	10.8	47.0	50	AAZ28696	Human SNP oligonuc
535	10.8	47.0	31	23	AB197849	Non-endogenous hum	608	10.8	47.0	50	AAZ29849	Human SNP oligonuc
536	10.8	47.0	32	21	AAV73111	Human MC1R gene re	c 609	10.8	47.0	50	AAZ30002	Human SNP oligonuc
537	10.8	47.0	32	21	AAZ88085	Human interleukin	610	10.8	47.0	50	AAZ34018	Human SNP oligonuc
538	10.8	47.0	32	21	AAZ58560	Human interleukin	611	10.8	47.0	50	AAZ34195	Human SNP oligonuc
539	10.8	47.0	32	21	AAZ29035	Txin 2 gene-specif	612	10.8	47.0	50	AAZ34547	Human SNP oligonuc
540	10.8	47.0	32	23	AB197850	Non-endogenous hum	c 613	10.8	47.0	50	AAI76887	Human silent SNP c
541	10.8	47.0	32	23	AB197851	Non-endogenous hum	614	10.8	47.0	50	AAH89831	Human coding sequ
542	10.8	47.0	33	15	AAQ70858	Foldback triplex-f	615	10.6	46.1	18	AAQ37154	Probe to detect GM
543	10.8	47.0	33	20	AAx60068	3' untranslated re	c 616	10.6	46.1	18	AAQ56863	PCR primer 17 for
544	10.8	47.0	34	17	AAV04400	PHENH6 primer #1.	c 617	10.6	46.1	18	AAI12894	Human RB1 (retinob
545	10.8	47.0	34	19	AAV00259	Cloned psi 10 prom	618	10.6	46.1	18	AAV08005	Probe GM-CSF for I
546	10.8	47.0	34	20	AAx01916	Bacteriophage T7 R	c 619	10.6	46.1	19	AAH89909	AE-labelled RNA pr
547	10.8	47.0	34	22	AAI66425	Kringle protein 13	c 620	10.6	46.1	19	AAZ11027	Probe #7 to detect
548	10.8	47.0	35	20	AAx57526	TGMV coat protein	c 621	10.6	46.1	19	AAZ11290	Mycobacterium aviu
549	10.8	47.0	36	20	AAx79331	P. furiosus endonuc	c 622	10.6	46.1	20	AAQ37772	HCY universal olig
550	10.8	47.0	36	22	AAV24447	C. thermomarginogen	c 623	10.6	46.1	20	AAQ080805	HCY genotype deter
551	10.8	47.0	36	22	AAV24449	C. thermomarginogen	c 624	10.6	46.1	20	AAQ76004	IRS-1 PCR primer.
552	10.8	47.0	36	22	AAV74289	Arabidopsis calcicu	625	10.6	46.1	20	AAZ03245	PCR primer used to
553	10.8	47.0	37	22	AAI14067	Vector pADAP/ST-AR	c 626	10.6	46.1	20	AAV45609	Primer for Mycobac
554	10.8	47.0	37	22	AAI14068	Vector pADAP/ST-AR	c 627	10.6	46.1	20	AAV45608	Primer for Mycobac
555	10.8	47.0	38	20	AAx19407	Rat polyome mRNA	c 628	10.6	46.1	20	AAZ44505	M. tuberculosis 16
556	10.8	47.0	39	15	AAQ70857	Foldback triplex-f	629	10.6	46.1	20	AAV72958	Human daxx inhibit
557	10.8	47.0	39	20	AAZ23561	RNAse T1 PCR prime	c 630	10.6	46.1	20	AAV91054	PCR primer for Hum
558	10.8	47.0	39	20	AAx35486	Upstream primer CT	c 631	10.6	46.1	20	AAI31802	Human RANK antisen
559	10.8	47.0	39	20	AAx26505	WO 9909191 SeqID #	c 632	10.6	46.1	20	ABF95386	Capture oligonucle
560	10.8	47.0	39	21	AAZ35580	Amplification prim	c 633	10.6	46.1	20	ABF95781	Capture oligonucle
561	10.8	47.0	40	18	AAV17339	Primer 96 used in	c 634	10.6	46.1	20	AAQ02830	Mycobacterium tube
562	10.8	47.0	40	18	AAV87163	IFN-gamma 2'F/NH2	635	10.6	46.1	21	AAQ40069	E. coli 16S rRNA o
563	10.8	47.0	40	22	AAV74442	PCR primer used to	c 636	10.6	46.1	21	AAV57651	Exon 9 of an ENAC
564	10.8	47.0	41	22	AAV50844	Maize polymorphic	637	10.6	46.1	21	AAI11075	Bacterial 16S RNA
565	10.8	47.0	41	19	AAV47702	Maize polymorphic	c 638	10.6	46.1	22	AAQ52620	Primer Y673S huHG
566	10.8	47.0	41	20	AAx19298	Human granulocyte	639	10.6	46.1	22	AAV72015	Primer detects mar
567	10.8	47.0	41	22	AAH48082	Ras GTPase-activat	640	10.6	46.1	22	AAV71943	Primer detects mar
568	10.8	47.0	42	19	AAV05421	Primer used in pro	c 641	10.6	46.1	22	AAV48447	Transforming growt
569	10.8	47.0	42	20	AAZ25254	Caspase-3 PCR prim	c 642	10.6	46.1	22	AAV15641	Primer used to gen
570	10.8	47.0	42	21	AAV72881	VEGF gene PCR prim	643	10.6	46.1	22	AAI66585	Gene typing PCR pr
571	10.8	47.0	42	21	AAV5854	VEGF PCR primer SE	c 644	10.6	46.1	22	AAI11298	Human ANK gene PCR
572	10.8	47.0	43	21	AAZ44610	Transcription vect	645	10.6	46.1	22	AAV89963	Human ANK gene PCR
573	10.8	47.0	43	22	AAV61144	B. napus HPPD PCR	c 646	10.6	46.1	23	AAV66556	PCR primer used to
574	10.8	47.0	44	19	AAV11490	A. niger transposa	c 647	10.6	46.1	23	AAI38492	Oligonucleotide 10
575	10.8	47.0	44	20	AAZ30897	Oligonucleotide WF	c 648	10.6	46.1	23	AAI11292	Human beta-globin
576	10.8	47.0	44	22	AAZ82186	Human retrovirus D	649	10.6	46.1	24	AAI36712	Human ANK gene PCR
577	10.8	47.0	45	19	AAV38167	Oligonucleotide-81	650	10.6	46.1	24	AAV00171	Downstream primer
578	10.8	47.0	45	19	AAV38168	Oligonucleotide-82	c 651	10.6	46.1	24	AAV00171	Human CD8 PCR anti
579	10.8	47.0	45	19	AAV11489	A. niger transposa	c 652	10.6	46.1	24	AB187342	Capture oligonucle
580	10.8	47.0	45	20	AAx82032	Mouse heavy chain	c 653	10.6	46.1	24	AB188132	Capture oligonucle
581	10.8	47.0	45	20	AAx2013	Mouse heavy chain	654	10.6	46.1	24	AB188133	Capture oligonucle
582	10.8	47.0	45	20	AAx05563	Mouse heavy chain	655	10.6	46.1	24	AB189176	Capture oligonucle
583	10.8	47.0	45	20	AAx03242	PCR primer used to	c 656	10.6	46.1	24	AB189177	Capture oligonucle
584	10.8	47.0	45	22	AAI01740	Exochitinase gene	c 657	10.6	46.1	25	AAV66555	Oligonucleotide 10
585	10.8	47.0	45	22	AAQ87059	Probe used to isol	c 658	10.6	46.1	25	AAI60406	Primer CRE3fused t
586	10.8	47.0	46	15	AAQ76948	Human genome fragm	659	10.6	46.1	25	AAI60589	Glomerular fibrone
587	10.8	47.0	46	16	AAQ84392	Mycobacterium smeg	c 660	10.6	46.1	25	AAI38491	Human beta-globin
588	10.8	47.0	46	19	AAV68584	Nucleotide sequenc	661	10.6	46.1	26	AAI1664	HCV(+)RNA oligonuc
589	10.8	47.0	46	19	AAV01774	C. trachomatis cry	662	10.6	46.1	27	AAQ24380	PCR primer C. Syn
590	10.8	47.0	46	20	AAV78455	Primer 2. Synthet	663	10.6	46.1	27	AAV19054	Tetracycline knock
591	10.8	47.0	46	20	AAx30266	Chlamydia cryptic	664	10.6	46.1	27	AAV68656	Nucleotide sequenc
592	10.8	47.0	46	20	AAx30007	Amplification prim	665	10.6	46.1	27	AAH43364	MIP-2 (antisense)
593	10.8	47.0	46	20	AAV82662	Amplification prim	666	10.6	46.1	27	AAZ25783	S. chrysomallus AC

c 667	10.6	46.1	28	16	AAQ94138	HML(R153A,R154A),	740	10.6	46.1	42	21	AAQ65243	Allele-specific st
c 668	10.6	46.1	29	16	AAQ94139	HML(R153A,R154A),	741	10.6	46.1	42	21	AAA65065	Exemplary DNA #3 e
c 669	10.6	46.1	28	20	AAAI6822	Aryl hydrocarbon n	742	10.6	46.1	42	22	AAQ63634	SDA primer haemsda
c 670	10.6	46.1	29	20	AAAI6995	Aryl hydrocarbon n	743	10.6	46.1	42	22	AAQ64894	Novel strand displ
c 671	10.6	46.1	29	20	AAAI9728	Integrin alpha 6 s	c 744	10.6	46.1	43	19	AAV33648	Plasmids pVLSNOSIB
c 672	10.6	46.1	29	21	AAA24229	Oestrogen receptor	745	10.6	46.1	43	19	AAV33646	Mouse VL30 promote
c 673	10.6	46.1	29	21	AAA04241	Polymorphic fragme	c 746	10.6	46.1	43	21	AAZ94644	Mutagenic primer H
c 674	10.6	46.1	29	21	AAA04563	Polymorphic fragme	747	10.6	46.1	43	21	AAZ94645	Mutagenic primer H
c 675	10.6	46.1	30	22	AAZ55487	Oligonucleotide RB	c 748	10.6	46.1	43	21	AAZ94645	Human alpha-3 IV c
c 676	10.6	46.1	30	22	AAZ54460	Primer used to gen	749	10.6	46.1	45	12	AAQ10551	Bone calcification
c 677	10.6	46.1	30	22	AAZ54468	Primer used to gen	c 750	10.6	46.1	45	20	AAZ32422	scFv 12B5 heavy ch
c 678	10.6	46.1	31	19	AAV19852	Primer for human 1	c 751	10.6	46.1	45	20	AAZ32425	PCR primer used to
c 679	10.6	46.1	31	19	AAV19852	EP-892047 Seq ID 2	752	10.6	46.1	45	21	AAZ94996	E. tenella small r
c 680	10.6	46.1	31	21	AAZ94375	Caenorhabditis ele	753	10.6	46.1	45	21	AAQ01235	Biotin-binding pep
c 681	10.6	46.1	31	22	AAI31153	Human single nucle	c 754	10.6	46.1	46	15	AAQ69394	Human growth hormo
c 682	10.6	46.1	32	15	AAQ63989	Mouse low-density	c 755	10.6	46.1	46	18	AAQ63856	Human growth hormo
c 683	10.6	46.1	32	16	AAQ03449	Human LAG-3 extrac	c 756	10.6	46.1	46	20	AAI17144	Test sequence from
c 684	10.6	46.1	33	13	AAQ31161	Probe 130 for geno	c 757	10.6	46.1	47	14	AAQ34665	H-ras sense primer
c 685	10.6	46.1	33	14	AAQ46467	Hepatitis C virus	c 758	10.6	46.1	47	14	AAQ46361	PCR sense primer t
c 686	10.6	46.1	33	19	AAV07841	HCV.33.12 amplifie	c 759	10.6	46.1	47	18	AAQ36445	PCR primer for H-r
c 687	10.6	46.1	33	20	AAV83069	Amplifier probe HC	c 760	10.6	46.1	47	19	AAV07874	H-ras gene sense p
c 688	10.6	46.1	33	22	AAH73956	Human molybdenum p	c 761	10.6	46.1	47	20	AAQ10299	PCR primer used to
c 689	10.6	46.1	33	22	AAQ89168	p-HVDE sequence fr	762	10.6	46.1	47	20	AAZ52585	Human genome blall
c 690	10.6	46.1	33	24	ABA05154	Human cannabinoid	c 763	10.6	46.1	47	20	AAI15089	PCR primer used to
c 691	10.6	46.1	34	19	AAV37234	PCR primer for mou	c 764	10.6	46.1	47	20	AAQ05489	Human H-ras gene f
c 692	10.6	46.1	34	20	AAZ52452	Forward PCR primer	c 765	10.6	46.1	47	21	AAZ68661	Human map-related
c 693	10.6	46.1	34	21	AAA46915	PCR primer used to	c 766	10.6	46.1	47	21	AAZ68991	Human map-related
c 694	10.6	46.1	34	22	AAZ72610	Human PRO polypept	c 767	10.6	46.1	47	21	AAH89913	Exemplary oligonuc
c 695	10.6	46.1	35	18	AAZ50850	Blocking oligonuc	c 768	10.6	46.1	47	21	AAZ48150	Human H-ras PCR pr
c 696	10.6	46.1	35	22	AAZ75846	Porcine circovirus	769	10.6	46.1	48	12	AAQ12252	HIV-1 LTR mutation
c 697	10.6	46.1	35	22	AAZ75846	PCV-1 virus ORF2 g	c 770	10.6	46.1	48	20	AAZ99203	M. dovis 16S rRNA
c 698	10.6	46.1	35	24	AAZ02829	Mycobacterium tube	c 771	10.6	46.1	48	20	AAZ99204	M. avium 16S rRNA
c 699	10.6	46.1	36	13	AAQ21153	Sequence of DNA do	c 772	10.6	46.1	48	20	AAZ99202	M. tuberculosis 16
c 700	10.6	46.1	36	18	AAZ91801	Target binding seq	c 773	10.6	46.1	48	22	AAZ85972	PRO cDNA amplifica
c 701	10.6	46.1	36	19	AAV20589	Bovine ADAM 10 PCR	774	10.6	46.1	49	16	AAQ98124	Label extender pro
c 702	10.6	46.1	36	20	AAZ87666	Hepatocyte growth	775	10.6	46.1	50	22	AAI27862	Human SNP oligonuc
c 703	10.6	46.1	36	20	AAZ73945	Human TNF-alpha co	776	10.6	46.1	50	22	AAI27863	Human SNP oligonuc
c 704	10.6	46.1	36	21	AAZ89286	Human tissue bindi	777	10.6	46.1	50	22	AAI28001	Human SNP oligonuc
c 705	10.6	46.1	36	22	AAH46635	DNA encoding flag	c 778	10.6	46.1	50	22	AAI30328	Human SNP oligonuc
c 706	10.6	46.1	37	18	AAZ79536	Jun leucine zipper	779	10.6	46.1	50	22	AAI32133	Human SNP oligonuc
c 707	10.6	46.1	37	22	AAZ75898	Human papillomavir	780	10.6	46.1	50	22	AAI32134	Human SNP oligonuc
c 708	10.6	46.1	38	14	AAQ36869	PCR primer for D.	781	10.6	46.1	50	22	AAI32421	Human SNP oligonuc
c 709	10.6	46.1	38	18	AAZ91804	Target binding seq	782	10.6	46.1	50	22	AAI33859	Human SNP oligonuc
c 710	10.6	46.1	39	19	AAV16821	Mycobacterium kans	783	10.6	46.1	50	22	AAI34612	Human SNP oligonuc
c 711	10.6	46.1	39	22	AAH41085	PCR primer specif	c 784	10.6	46.1	50	22	AAH20061	Human SNP oligonuc
c 712	10.6	46.1	40	17	AAZ37089	ElAF matrix metall	785	10.6	46.1	50	22	AAH20061	M. avium 16S rRNA
c 713	10.6	46.1	40	18	AAZ90816	Primer P2 for C. p	c 786	10.6	46.1	50	22	AAH20061	Probe used to iden
c 714	10.6	46.1	40	19	AAV16820	Mycobacterium kans	c 787	10.6	46.1	50	22	AAV63773	Human JAGGED1 exon
c 715	10.6	46.1	40	21	AAZ87834	Amplification prim	c 788	10.6	46.1	50	22	AAV62568	Substrate for HH r
c 716	10.6	46.1	40	21	AAZ87839	HRP conjugated P2	789	10.6	46.1	50	22	AAQ76214	HSV L/ST primer.
c 717	10.6	46.1	40	21	AAZ46372	PCR primer used to	790	10.6	46.1	50	22	AAV72572	Thyroid peroxidase
c 718	10.6	46.1	40	21	AAZ46374	Oligonucleotide pr	791	10.6	46.1	50	22	AAZ89345	Human UCP3 protein
c 719	10.6	46.1	40	21	AAZ95917	Polynucleotide seq	792	10.6	46.1	50	22	ABA81947	Rat G-protein sero
c 720	10.6	46.1	40	22	AAI14554	Arabidopsis thalia	793	10.6	46.1	50	22	AAH62996	Angiotensinogen mo
c 721	10.6	46.1	40	22	AAI14567	Arabidopsis thalia	794	10.6	46.1	50	22	AAV85725	LRP5 exon primer E
c 722	10.6	46.1	40	22	AAZ07859	Binding site selec	795	10.6	46.1	50	22	AAV23973	Primer for detecti
c 723	10.6	46.1	40	22	AAZ07872	Binding site selec	796	10.6	46.1	50	22	AAI11896	PCR primer used to
c 724	10.6	46.1	40	22	AAI10613	DNA ligand #19 for	797	10.6	46.1	50	22	AAZ60310	Human MDMX antisen
c 725	10.6	46.1	40	22	AAZ08927	Arabidopsis thalia	c 798	10.6	46.1	50	22	AAZ60310	Forward primer spe
c 726	10.6	46.1	40	22	AAZ08940	Arabidopsis thalia	799	10.6	46.1	50	22	AAZ38440	Human angiotensino
c 727	10.6	46.1	40	22	AAZ03339	A group IA abscisi	c 800	10.6	46.1	50	22	AAH76267	Human adenosine A2
c 728	10.6	46.1	40	22	AAZ03332	ABRE binding seque	801	10.6	46.1	50	22	AAH42437	PCR primer used to
c 729	10.6	46.1	40	22	AAZ00392	ABRE binding seque	802	10.6	46.1	50	22	AAH67110	Human angiotensino
c 730	10.6	46.1	40	22	AAZ00405	PCR primer OPR136	803	10.6	46.1	50	22	ABZ97356	Capture oligonucle
c 731	10.6	46.1	41	17	AAZ34716	Human diacylglycer	c 804	10.6	46.1	50	22	AAI17756	Oligo #27 for ampl
c 732	10.6	46.1	41	22	AAH46537	Human peroxidase a	c 805	10.6	46.1	50	22	AAZ80173	Forward primer #44
c 733	10.6	46.1	41	22	AAI54912	Guinea pig histami	806	10.6	46.1	50	22	AAZ76046	Human prostate spe
c 734	10.6	46.1	41	24	AAI71001	Human G2 activati	807	10.6	46.1	50	22	AAZ76055	Human prostate spe
c 735	10.6	46.1	41	24	ABA92344	Ribosomal S3 prote	808	10.6	46.1	50	22	AAZ93746	Drosophila Na+ dri
c 736	10.6	46.1	41	24	ABA04976	Novel strand displ	809	10.6	46.1	50	22	AAZ07187	Anchored PCR prim
c 737	10.6	46.1	42	21	AAZ63153	Novel strand displ	810	10.6	46.1	50	22	AAH42163	PCR primer for cDN
c 738	10.6	46.1	42	21	AAZ64832	Novel strand displ	811	10.6	46.1	50	22	AAH62434	Cholinergic recept
c 739	10.6	46.1	42	21	AAZ65176	Novel strand displ	c 812	10.6	46.1	50	22	AAZ97279	Human gene single

813	10.4	45.2	21	22	AAF97630	Human gene single	c 886	10.4	45.2	30	20	AAx85758	PCR primer used to
814	10.4	45.2	21	22	AAF59583	Mouse urotensin II	c 887	10.4	45.2	30	20	AAx85761	PCR primer used to
c 815	10.4	45.2	21	22	ABA10180	Tail primer #173 f	888	10.4	45.2	30	20	AAx58601	Human cancer anti
c 816	10.4	45.2	22	16	AAAT05920	COX II sense probe	889	10.4	45.2	30	21	AAx30700	Human HG38 (V765K)
818	10.4	45.2	22	18	AAAT76319	Human muscarinic a	890	10.4	45.2	30	21	AAx294325	Rat neurotensin Nr
819	10.4	45.2	22	20	AAZ25147	Human short inters	c 891	10.4	45.2	30	21	AAZ61196	Probe C12C151 use
820	10.4	45.2	22	20	AAZ25157	Human short inters	c 892	10.4	45.2	30	22	AAx5831	Primer #3 used in
821	10.4	45.2	22	20	AAZ25158	Human short inters	c 893	10.4	45.2	30	22	AAx77267	Primer X specific
c 822	10.4	45.2	22	21	AAx54117	Muscarinic acetylch	c 894	10.4	45.2	30	22	AAx31885	Hamster Ku86 PCR p
c 823	10.4	45.2	22	21	AAx80174	Forward primer #45	c 895	10.4	45.2	31	14	AAQ51483	Dengue virus sequ
c 824	10.4	45.2	22	21	AAx19683	Human muscarinic a	c 896	10.4	45.2	31	20	AAZ23224	HCV NS5B DNA speci
825	10.4	45.2	22	21	AAx75912	PCR primer for CDN	c 897	10.4	45.2	31	21	AAx78849	Human genomic DNA
826	10.4	45.2	22	21	AAx76047	Human prostate spe	898	10.4	45.2	31	21	AAx58369	PCR primer pCDNA(S
827	10.4	45.2	22	21	AAx76060	Human prostate spe	899	10.4	45.2	31	22	AAI30457	Human single nucle
c 828	10.4	45.2	22	21	AAx33561	Low adenosine anti	900	10.4	45.2	31	22	AAI30458	Human single nucle
c 829	10.4	45.2	22	21	AAx50750	3'HUMAN OCR10rc pr	901	10.4	45.2	31	22	AAI30552	Human single nucle
c 830	10.4	45.2	22	22	AAH74132	Oligonucleotide #5	902	10.4	45.2	32	15	AAQ67142	Primer for amplify
c 831	10.4	45.2	22	23	AAH50117	Bacterial 23S/5S R	c 903	10.4	45.2	32	15	AAQ71642	Apo-B RNA editing
c 832	10.4	45.2	23	17	AAAT35856	3' PCR-RFLP modifi	c 904	10.4	45.2	32	15	AAQ87875	Component B gene p
c 833	10.4	45.2	23	18	AAAT59518	Prostate-specific	905	10.4	45.2	32	16	AAAT00830	HIV-1 HXB2 envelop
c 834	10.4	45.2	23	18	AAAT59518	Porcine CD34 forwa	c 906	10.4	45.2	32	16	AAQ84709	Non-specific unive
c 835	10.4	45.2	23	18	AAAT59518	Forward primer #46	907	10.4	45.2	32	17	AAAT32896	Human immunodefici
c 836	10.4	45.2	24	18	AAAT78855	340 bp 5' lecithin	c 908	10.4	45.2	32	17	AAAT42572	Primer #3 for acut
c 837	10.4	45.2	24	19	AAV38028	SCPEO section 3 co	909	10.4	45.2	32	17	AAAT35019	TIMP-1/fibronectin
c 838	10.4	45.2	24	19	AAV38029	SCPEO section 3 co	c 910	10.4	45.2	32	18	AAAT64570	Primer for thymus
c 839	10.4	45.2	24	19	AAV26275	T. vaginalis homoc	911	10.4	45.2	32	18	AAAT84458	Heat shock protein
c 840	10.4	45.2	24	21	AAx80176	Oligonucleotide us	c 912	10.4	45.2	32	19	AAV41631	Nucleotide sequenc
841	10.4	45.2	24	21	AAx80176	Forward primer #47	c 913	10.4	45.2	32	20	AAx87365	Universal adaptor
842	10.4	45.2	24	21	AAx93970	Primer used to gen	c 914	10.4	45.2	32	20	AAx22978	Canine En-2 primer
c 843	10.4	45.2	24	21	AAx89689	Human ADAM DNA PCR	c 915	10.4	45.2	32	20	AAx06681	Antisense universa
c 844	10.4	45.2	24	21	AAx39745	Human glycerinalde	c 916	10.4	45.2	32	21	AAx96949	RACE PCR primer us
c 845	10.4	45.2	24	22	AAx30649	Human HDGFX hybrid	c 917	10.4	45.2	32	21	AAx64094	Universal adapter
c 846	10.4	45.2	24	22	AAx30652	Human HDGFX hybrid	c 918	10.4	45.2	32	21	AAx88573	Universal amplific
c 847	10.4	45.2	24	22	AAx25450	Oligonucleotide us	c 919	10.4	45.2	32	21	AAx51130	Universal amplific
c 848	10.4	45.2	24	24	AB184780	Capture oligonucle	c 920	10.4	45.2	32	21	AAx251139	Soluble herpesviru
c 849	10.4	45.2	24	24	AB184781	Capture oligonucle	921	10.4	45.2	32	21	AAH22975	Human IL-6 promote
850	10.4	45.2	24	24	AB186024	Capture oligonucle	c 922	10.4	45.2	32	22	AAH25201	Primer used to amp
c 851	10.4	45.2	24	24	AB186025	Capture oligonucle	c 923	10.4	45.2	32	22	AAH04959	Human homologous p
c 852	10.4	45.2	24	24	AB191282	Capture oligonucle	c 924	10.4	45.2	32	22	AAH12938	Rainbow trout prep
c 853	10.4	45.2	24	24	AB191283	Capture oligonucle	925	10.4	45.2	33	13	AAQ31115	Probe 84 specific
c 854	10.4	45.2	25	18	AAQ37580	HCV conserved regi	926	10.4	45.2	33	13	AAQ31115	Probe 126 for geno
c 855	10.4	45.2	25	19	AAV53717	Hepatitis C virus	927	10.4	45.2	33	14	AAQ46421	Hepatitis C virus
c 856	10.4	45.2	25	19	AAV53718	Nucleotide sequenc	928	10.4	45.2	33	14	AAQ46463	Hepatitis C virus
c 857	10.4	45.2	25	19	AAV53717	Forward primer #48	929	10.4	45.2	33	19	AAV07837	HCV 33.8 amplifier
c 858	10.4	45.2	26	14	AAQ37585	HCV conserved regi	930	10.4	45.2	33	21	AAH3065	Amplifier probe HC
c 859	10.4	45.2	26	18	AAAT64899	Sequence of PCR pr	931	10.4	45.2	33	21	AAZ35996	CAT gene long rang
c 860	10.4	45.2	26	21	AAx89839	Hepatitis C virus	c 932	10.4	45.2	33	22	AAx84175	Human OATP-B PCR p
c 861	10.4	45.2	26	21	AAx89839	Primer od53. Synt	c 933	10.4	45.2	34	15	AAQ55228	Full length CD40 b
c 862	10.4	45.2	26	22	AAx12757	PCR primer oligonu	c 934	10.4	45.2	34	16	AAQ96202	Primer #2. Synthe
c 863	10.4	45.2	26	22	AAI65053	PCR primer #4. Un	935	10.4	45.2	34	16	AAQ88949	VEGF RNA nucleic a
c 864	10.4	45.2	27	9	AAH81250	Probe O-34BHI to i	936	10.4	45.2	34	17	AAAT36515	Primer to amplify
c 865	10.4	45.2	27	9	AAH81250	Probe O-34BHI for	c 937	10.4	45.2	34	18	AAAT79187	Human full length
c 866	10.4	45.2	27	14	AAQ36549	Encodes Arg rich i	c 938	10.4	45.2	34	20	AAx36577	PCR primer for hum
c 867	10.4	45.2	27	20	AAx58602	Human cancer anti	c 939	10.4	45.2	34	22	AAx13973	Shope Fibroma Viru
c 868	10.4	45.2	27	22	AAH42310	Primer for DNA enc	940	10.4	45.2	34	22	AAAD07438	Kaposi's sarcoma v
c 869	10.4	45.2	27	22	AAH19828	Synthetic DNA for	941	10.4	45.2	34	22	AAx00266	LPA receptor-relat
c 870	10.4	45.2	27	22	AAH19829	Synthetic DNA for	c 942	10.4	45.2	36	19	AAV45087	Human IL-12 primer
c 871	10.4	45.2	27	22	AAx30468	RT-PCR primer BA-F	c 943	10.4	45.2	36	21	AAx35922	Permutin linker e
c 872	10.4	45.2	27	22	AAx30469	RT-PCR primer BA-R	c 944	10.4	45.2	37	16	AAQ88954	VEGF RNA nucleic a
873	10.4	45.2	27	22	AAx24392	M tuberculosis Rv2	c 945	10.4	45.2	37	19	AAV26166	PRRS ORF2 gene PCR
874	10.4	45.2	28	22	AAx59949	Canine IgG heavy c	946	10.4	45.2	37	22	AAH91190	Human inflammatory
875	10.4	45.2	28	22	AAH28148	PCR primer used to	c 947	10.4	45.2	37	22	AAx30198	Clone 11618130.0.2
876	10.4	45.2	29	20	AAx84022	PCR primer for HCV	c 948	10.4	45.2	37	22	AAx26091	Feline IL-12p35 PC
c 877	10.4	45.2	29	20	AAx84023	PCR primer for HCV	949	10.4	45.2	38	18	AAx66670	Mycobacterium kans
c 878	10.4	45.2	29	21	AAx00251	Hammerhead ribozym	950	10.4	45.2	38	19	AAx85726	LRP5 exon primer E
c 879	10.4	45.2	29	21	AAx58398	Human VNTK5 PCR pr	951	10.4	45.2	38	20	AAZ00736	S. agalactiae GBS3
c 880	10.4	45.2	29	21	AAx04121	Polymorphic fragme	952	10.4	45.2	38	20	AAx24243	Oligonucleotide pr
881	10.4	45.2	29	21	AAx36824	Probe TUB-1 used t	953	10.4	45.2	38	20	AAx24259	Oligonucleotide pr
882	10.4	45.2	29	22	AAx43955	Plasmid PBS-RSV mu	c 954	10.4	45.2	38	21	AAx49338	Primer used to amp
c 883	10.4	45.2	29	22	AAx25791	S. chrysomallus AC	c 955	10.4	45.2	38	22	AAH15528	Beta actin gene pr
884	10.4	45.2	29	22	AAI65151	Canine IL12p35 gen	956	10.4	45.2	38	22	AAH96845	Human Chk1 ribozym
885	10.4	45.2	29	23	AB197681	Endogenous human G	957	10.4	45.2	38	22	AAH96944	Human NOGO Zinzyne
			30	19	AAV66536	Reverse PCR primer	958	10.4	45.2	38	23	ABK05624	Human NOGO Zinzyne

CC treatment of tumors, autoimmune diseases, scar formation, inflammation,
 CC allergy, rheumatic diseases and defence against transplantation.
 CC AAZ43869-Z43871 represent primers described in the method of the
 CC invention.
 XX
 SQ Sequence 23 BP; 4 A; 7 C; 8 G; 4 T; 0 other;

Query Match 100.0%; Score 23; DB 21; Length 23;
 Best Local Similarity 100.0%; Pred. No. 0.096;
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 accaggcgtctcgtggccacat 23
 |||||
 Db 23 ACCAGGCTCTCGTGGCCACAT 1

RESULT 3
 AAQ58903
 ID AAQ58903 standard; DNA; 48 BP.

XX AC AAQ58903;
 XX
 DT 26-OCT-1994 (first entry)

XX Human beta-glucuronidase cloning oligonucleotide Hum.B-Gluc back.
 DE
 XX Carcinoembryonic antigen; single chain variable region; sfv fragment;
 KW fusion gene; cancer treatment; targeted drug delivery; tumour;
 KW beta-glucuronidase; prodrug activating enzyme; ss.
 XX

OS Synthetic.
 XX
 PN EP590530-A.
 XX
 PD 06-APR-1994.
 XX
 PF 24-SEP-1993; 93EP-0115418.
 XX
 PR 02-OCT-1992; 92DE-4233152.
 XX
 PA (BEHW) BEHRINGWERKE AG.

XX Bosslet K, Czech J, Gehrman M, Seemann G;
 XX
 DR WPI; 1994-111012/14.
 XX
 PT New fusion protein contg. enzyme for prodrug activation - coupled
 PT to antigen binding component, esp. sfv antibody fragment, partic.
 PT for treatment of tumours
 XX

PS Example 10; Page 20; 35pp; German.
 XX
 CC Oligonucleotides Hum.B-Gluc back (AAQ58903) and Hum.B-Gluc for
 CC (AAQ58904) were used for cloning the human beta-glucuronidase gene into
 CC a pUC19 vector all ready containing an anti-CEA single chain antibody
 CC construct sfv 431/26. The resultant fusion protein is useful for
 CC targeting beta-glucuronidase to cancer cells expressing CEA, where
 CC the enzyme is able to convert a prodrug into its active form.
 XX

SQ Sequence 48 BP; 14 A; 11 C; 16 G; 7 T; 0 other;

Query Match 63.5%; Score 14.6; DB 15; Length 48;
 Best Local Similarity 81.0%; Pred. No. 1e+03;
 Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 ccaggcgtctcgtggccaca 22
 |||||
 Db 12 caaagcgtcgtggccaca 32

RESULT 4

AAQ04776/c
 ID AAX04776 standard; DNA; 30 BP.
 XX
 AC AAX04776;
 XX
 DT 09-APR-1999 (first entry)

XX PCR primer of the invention.
 DE
 XX Acremonium sp. S4G13; glucose transfer; sugar transferase
 KW sugar receptor; starch; PCR primer; ss.
 KW
 XX Synthetic.
 OS

XX JP11009276-A.
 PN
 XX
 PD 19-JAN-1999.

XX 19-JUN-1997; 97JP-0163110.
 PF
 XX 19-JUN-1997; 97JP-0163110.

XX (KIRI) KIRIN BREWERY KK.
 PA
 XX WPI; 1999-145893/13.

XX New sugar transferase gene and enzyme - useful for catalysing the
 XX transfer of an alpha-1 right arrow 3 bond to a sugar receptor for
 PT saccharide preparation
 XX

PS Example 6; Page 11; 20pp; Japanese.

XX The present PCR primer was used in the course of the invention. The
 CC specification describes a sugar transferase protein of Acremonium
 CC sp. S4G13. The protein preferably catalyses the glucose transfer of an
 CC alpha-1 right arrow 3 bond or the glucose transfer of an alpha-1 right
 CC arrow 3 and an alpha-1 right arrow 4 bond to a sugar receptor by
 CC reacting with a substrate selected from starch and its decomposition
 CC products.
 XX

SQ Sequence 30 BP; 5 A; 12 C; 8 G; 5 T; 0 other;

Query Match 61.7%; Score 14.2; DB 20; Length 30;
 Best Local Similarity 84.2%; Pred. No. 1.5e+03;
 Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 accaggcgtctcgtggccc 19
 |||||
 Db 25 ACCAGGCTTTCGTGGGCC 7

RESULT 5
 AAL28873/c
 ID AAL28873 standard; DNA; 50 BP.

XX AAL28873;
 AC

DT 24-JAN-2002 (first entry)

XX Human SNP oligonucleotide #2081.

XX Immunosuppressive; immunostimulatory; antiinflammatory; cytostatic;
 KW neuroprotective; antimicrobial; gene therapy; vaccine; amylase; cancer;
 KW amyloid protein; angiotensin; apoptosis related protein; cadherin;
 KW cyclin; polymerase; oncogene; histone; kinase; colony stimulating factor;
 KW complement related protein; cytochrome; cytochrome; interferon;
 KW interleukin; G-protein coupled receptor; thioesterase; inflammation;
 KW multifactorial disease; autoimmune disease; infection;
 KW nervous system disease; ss.

XX Homo sapiens.

XX OS

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PN WO200147944-A2.
XX
PD 05-JUL-2001.
XX
PF 28-DEC-2000; 2000WO-US35498.
XX
PR 28-DEC-1999; 99US-0173419.
XX
PR 27-DEC-2000; 2000US-0173419.
XX
PA (CURA-) CURAGEN CORP.
XX
PI Shimkets RA, Leach M;
XX
PI WPI; 2001-465210/50.
XX
DR Polymorphic nucleic acids encoding e.g. amylases, cyclins, polymerases,
XX oncogenes and histones, useful for diagnosing and treating, e.g.
PT cancer, autoimmune diseases and infections -
PT
PT
PS Claim 1; Page 1977; 4143pp; English.
XX
CC The present invention relates to oligonucleotides encoding polymorphic
CC variants of proteins related to amylases, amyloid proteins, angiotensin,
CC apoptosis related proteins, cadherin, cyclin, cyclin, polymerase, oncogenes,
CC histones, kinases, colony stimulating factors, complement related
CC proteins, cytochromes, kinesins, cytokines, interferons, interleukins,
CC G-protein coupled receptors and thioesterases. The present sequence is
CC one such oligonucleotide. The oligonucleotides and the peptides encoded
CC by them may be used in the prevention, diagnosis and treatment of
CC diseases associated with inappropriate expression of the proteins listed
CC above. Disorders that may be prevented, diagnosed and/or treated include
CC multifactorial diseases with a genetic component, such as autoimmune
CC diseases (e.g. rheumatoid arthritis, multiple sclerosis, diabetes,
CC systemic lupus erythematosus and Grave's disease), inflammation, cancer
CC (e.g. cancers of the bladder, brain, breast, colon and kidney,
CC leukaemia), diseases of the nervous system and an infection of pathogenic
CC organisms.
XX
SQ Sequence 50 BP; 9 A; 17 C; 19 G; 5 T; 0 other;

Query Match 60.9%; Score 14; DB 22; Length 50;
Best Local Similarity 77.3%; Pred. No. 2e+03;
Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 2 ccaggcgtctcgtggccacat 23
    |||| || | |||| || |||
Db 35 CCAGCGCGCGGTGGCCCTCAT 14

RESULT 6
AAL28874/c
ID AAL28874 standard; DNA; 50 BP.
XX
AC AAL28874;
XX
DT 24-JAN-2002 (first entry)
XX
DE Human SNP oligonucleotide #2082.
XX
KW Immunosuppressive; immunostimulatory; antiinflammatory; cytostatic;
KW neuroprotective; antimicrobial; gene therapy; vaccine; amylase; cancer;
KW amyloid protein; angiotensin; apoptosis related protein; cadherin;
KW cyclin; polymerase; oncogene; histone; kinase; colony stimulating factor;
KW complement related protein; cytochrome; kinesin; cytokine; interferon;
KW interleukin; G-protein coupled receptor; thioesterase; inflammation;
KW multifactorial disease; autoimmune disease; infection;
KW nervous system disease; ss.
XX
OS Homo sapiens.
XX
PN WO200147944-A2.
XX

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PD 05-JUL-2001.
XX
PF 28-DEC-2000; 2000WO-US35498.
XX
PR 28-DEC-1999; 99US-0173419.
XX
PR 27-DEC-2000; 2000US-0173419.
XX
PA (CURA-) CURAGEN CORP.
XX
PI Shimkets RA, Leach M;
XX
PI WPI; 2001-465210/50.
XX
DR Polymorphic nucleic acids encoding e.g. amylases, cyclins, polymerases,
XX oncogenes and histones, useful for diagnosing and treating, e.g.
PT cancer, autoimmune diseases and infections -
PT
PT
PS Claim 1; Page 1977; 4143pp; English.
XX
CC The present invention relates to oligonucleotides encoding polymorphic
CC variants of proteins related to amylases, amyloid proteins, angiotensin,
CC apoptosis related proteins, cadherin, cyclin, cyclin, polymerase, oncogenes,
CC histones, kinases, colony stimulating factors, complement related
CC proteins, cytochromes, kinesins, cytokines, interferons, interleukins,
CC G-protein coupled receptors and thioesterases. The present sequence is
CC one such oligonucleotide. The oligonucleotides and the peptides encoded
CC by them may be used in the prevention, diagnosis and treatment of
CC diseases associated with inappropriate expression of the proteins listed
CC above. Disorders that may be prevented, diagnosed and/or treated include
CC multifactorial diseases with a genetic component, such as autoimmune
CC diseases (e.g. rheumatoid arthritis, multiple sclerosis, diabetes,
CC systemic lupus erythematosus and Grave's disease), inflammation, cancer
CC (e.g. cancers of the bladder, brain, breast, colon and kidney,
CC leukaemia), diseases of the nervous system and an infection of pathogenic
CC organisms.
XX
SQ Sequence 50 BP; 9 A; 16 C; 19 G; 6 T; 0 other;

Query Match 60.9%; Score 14; DB 22; Length 50;
Best Local Similarity 77.3%; Pred. No. 2e+03;
Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 2 ccaggcgtctcgtggccacat 23
    |||| || | |||| || |||
Db 34 CCAGCGCGCGGTGGCCCTCAT 13

RESULT 7
AAQ79883/c
ID AAQ79883 standard; cDNA; 34 BP.
XX
AC AAQ79883;
XX
DT 17-JUL-1995 (first entry)
XX
DE Adrenodoxin-reductase primer 8.
XX
KW P450sc; P450 side chain cleavage enzyme; fusion enzyme;
KW electron-transfer protein; transgenic animal; cholesterol;
KW atherosclerosis; adrenodoxin-reductase; AdRed; adrenodoxin; Adx;
KW polymerase chain reaction; PCR; amplification; primer; ss.
XX
OS Synthetic.
XX
PN WO9429434-A.
XX
PD 22-DEC-1994.
XX
XX
XX 09-JUN-1994; 94WO-US06698.
XX
XX 09-JUN-1993; 93US-0075193.
XX

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PA (REGC) UNIV CALIFORNIA.
 XX Black SM, HariKrishna JA, Miller WL;
 XX WPI; 1995-036464/05.
 XX Fusion enzyme comprising P450sc and an electron-transfer protein
 PT - used in the production of transgenic livestock with reduced
 PT cholesterol meat
 XX Example 1; Page 37; 91pp; English.
 XX The primers given in AAQ79878-85 were used to engineer human cDNAs
 CC for P450sc, adrenodoxin-reductase (AdRed) and adrenodin (Adx) for
 CC the construction of P450sc-AdRed, P450sc-Adx-AdRed and
 CC P450sc-AdRed-Adx fusion enzymes capable of cholesterol disposal.
 CC AdRed cDNA is amplified using primers 5-8 (AAQ79880-83,
 CC respectively).
 XX Sequence 34 BP; 4 A; 10 C; 16 G; 4 T; 0 other;
 SQ

Query Match 60.0%; Score 13.8; DB 16; Length 34;
 Best Local Similarity 88.2%; Pred. No. 2.4e+03;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 6 gcgtctcgtgggcaca 22
 ||| ||| ||| ||| ||| |||
 Db 32 GCGCCTCTGTGGCCACA 16

RESULT 8
 ID AAZ65685/C
 XX AAZ65685 standard; DNA; 47 BP.
 AC AAZ65685;
 XX
 XX 11-SEP-2001 (first entry)
 XX Human map-related biallelic marker SEQ ID NO:32.
 DE
 XX Human genome; biallelic marker; high density disequilibrium map;
 KW genomic map; haplotype; phenotype; polymorphic base; genotyping;
 KW haplotyping; hybridisation; identification; characterisation;
 KW diagnosis; single nucleotide polymorphism; SNP; ds.
 XX Homo sapiens.
 OS
 XX
 FH Key Location/Qualifiers
 FT variation replace(24,C)
 FT /*tag= a
 FT /standard_name= "single nucleotide polymorphism"
 XX
 PN WO954500-A2.
 XX
 XX 28-OCT-1999.
 PD
 XX
 XX 21-APR-1999; 99MO-IB00822.
 PF
 XX
 XX 21-APR-1998; 98US-0082614.
 PR
 XX 23-NOV-1998; 98US-0109732.
 PR
 XX (GEST) GENSET.
 PA
 XX Cohen D, Blumenfeld M, Chumakov I;
 PI
 XX WPI; 2000-013267/01.
 DR
 XX Novel biallelic markers used to construct a high density disequilibrium
 PT map of the human genome
 XX
 XX Claim 1; Page 237; 2745pp; English.
 PS
 XX

CC AAZ65654 to AAZ69578 represent human biallelic markers from the present
 CC invention, which contain a polymorphic base at position 24 of their
 CC nucleotide sequences. AAZ69579 to AAZ77440 represent amplification
 CC primers for the biallelic markers. The biallelic markers of the
 CC invention have a variety of uses: they can be used for high density
 CC mapping of the human genome, and in complex association studies and
 CC haplotyping studies which are useful in determining the genetic basis
 CC for disease states. Compositions and methods of the invention can also
 CC be useful for the identification of the targets for the development of
 CC pharmaceutical agents and diagnostic methods, as well as the
 CC characterisation of the differential efficacious responses to and side
 CC effects from pharmaceutical agents acting on a disease as well as other
 CC treatment.
 CC N.B. The SEQ ID NOS 2852, 2913, 2974, 3035, 3096, 3157, 3227, 3297
 CC and 3367, are not actually given a sequence in the Sequence Listing
 CC from the present invention.
 XX
 SQ Sequence 47 BP; 16 A; 10 C; 13 G; 8 T; 0 other;
 SQ

Query Match 60.0%; Score 13.8; DB 21; Length 47;
 Best Local Similarity 88.2%; Pred. No. 2.5e+03;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 6 gcgtctcgtgggcaca 22
 ||| ||| ||| ||| ||| |||
 Db 28 GCTTCTCTGTGGCCACA 12

RESULT 9
 ID AAQ58908
 XX AAQ58908 standard; DNA; 48 BP.
 AC AAQ58908;
 XX
 XX 26-OCT-1994 (first entry)
 DT
 XX
 DE E.coli beta-glucuronidase cloning oligonucleotide E.coli-B-Gluc.back.
 XX
 KW Carcinobryonic antigen; single chain variable region; sfv fragment;
 KW fusion gene; cancer treatment; targetted drug delivery; tumour;
 KW Escherichia coli; beta-glucuronidase; prodrug activating enzyme; ss.
 OS Synthetic.
 XX
 XX EP590530-A.
 PN
 XX
 PD 06-APR-1994.
 XX
 XX 24-SEP-1993; 93EP-0115418.
 PF
 XX
 XX 02-OCT-1992; 92DE-4233152.
 PR
 XX (BEHW) BEHRINGERWERKE AG.
 PA
 XX
 XX Bosslet K, Czech J, Gehrman M, Seemann G;
 PI
 XX WPI; 1994-111012/14.
 DR
 XX New fusion protein contg. enzyme for prodrug activation - coupled
 PT to antigen binding component, esp. sfv antibody fragment, partic.
 PT for treatment of tumours
 PT
 XX Example 10; Page 21; 35pp; German.
 PS
 XX Oligonucleotides E.coli-B-Gluc.for (AAQ58907) and E.coli-B-Gluc.back
 CC (AAQ58908) were used for cloning the E.coli beta-glucuronidase gene
 CC into a pUC19 vector all ready containing an anti-CEA single chain
 CC antibody construct sfv 431/26. The resultant fusion protein is useful
 CC for targetting beta-glucuronidase to cancer cells expressing CEA,
 CC where the enzyme is able to convert a prodrug into its active form.
 XX
 XX Sequence 48 BP; 14 A; 14 C; 12 G; 8 T; 0 other;
 SQ


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AC AAV64130;
XX
DT 25-JAN-1999 (first entry)
XX
DE Bovine beta-mannosidase PCR antisense primer MJ-125.
XX
KW Bovine; beta-mannosidase; beta-mannosidosis; diagnosis; goat; cattle;
KW primary storage product; tremor; deafness; dysmyelination; PCR primer;
KW ss.
XX
OS Synthetic.
OS Bos taurus.
XX
XX US5837836-A.
XX
XX 17-NOV-1998.
XX
XX 19-SEP-1995; 95US-0530524.
XX
XX 15-SEP-1994; 94US-0306546.
XX
XX 19-SEP-1995; 95US-0530524.
XX
XX (UNMS ) UNIV MICHIGAN STATE.
XX
XX Cavanagh KT, Chen H, Friderici K, Jones MZ;
PI WPI; 1999-023539/02.
XX
XX Bovine beta-mannosidase nucleic acid sequence and mutation(s) -
XX useful for diagnosis of the disease beta-mannosidosis and its
XX carriers
XX
XX Example 2; Column 18; 39pp; English.
XX
XX The present sequence represents a PCR primer for bovine beta-mannosidase.
XX The present invention also describes a nucleic acid molecule encoding
XX bovine beta-mannosidase, but where the adenine at position 2648 is
XX replaced by guanine. The nucleic acid is useful for the detection of the
XX disease beta-mannosidosis. This is an autosomal recessive inherited
XX disorder affecting mainly goats and cattle, caused a defect in the
XX enzyme beta-mannosidase. This mutation renders the afflicted animals
XX incapable of correctly processing primary storage products, resulting in
XX tremors, deafness and dysmyelination amongst other symptoms. The nucleic
XX acid is used in hybridisation assays, or other nucleic acid based assays
XX (e.g. PCR or restriction mapping) to detect beta-mannosidase, especially
XX where nucleic acid encoding bovine beta-mannosidase contains the adenine
XX to guanine mutation at position 2648, for specific detection of the
XX disease. The nucleic acid allows specific detection of presence or
XX absence of the disease. Previous detection methods relied on enzyme
XX activity assays which can be inaccurate as the range of activities
XX greatly varies from one individual to another, especially when tested
XX for in cross-breeds.
XX
XX Sequence 20 BP; 7 A; 5 C; 5 G; 3 T; 0 other;

Query Match 59.1%; Score 13.6; DB 20; Length 20;
Best Local Similarity 80.0%; Pred. No. 2.9e+03;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 4 aggcgtctcgtggccacat 23
DB 20 AGGTGTCGCTTAGCCACTT 1

RESULT 13
AAQ63451
ID AAQ63451 standard; DNA; 45 BP.
XX
XX AAQ63451;
XX
XX 18-NOV-1994 (first entry)
XX
```

```
DE REI human Ab L chain variable region synthetic fragment.
XX
XX Monoclonal antibody; Ab; ganglioside GM2; chimera;
KW chimeric antibody; expression vector; heavy; light; chain;
KW hypervariable region; CDR; constant region; hybridoma;
KW 19; immunoglobulin; promoter; enhancer; ds.
XX
OS Synthetic.
XX
XX AU9346181-A.
XX
XX 17-MAR-1994.
XX
XX 07-SEP-1993; 93AU-0046181.
XX
XX 07-SEP-1992; 92JP-0238452.
XX
XX (KYOW ) KYOWA HAKKO KOGYO KK.
XX
XX Hanai N, Hasegawa M, Koike M, Kuwana Y, Nakamura K;
XX Shitara K;
XX WPI; 1994-126857/16.
XX
XX Humanised antibody specific for ganglioside GM2 - used for
XX producing a cytotoxic effect on cancers such as melanoma,
XX neuroblastoma and glioma.
XX
XX Example 2; Page 121; 191pp; English.
XX
XX REI was used as human Ab L chain variable region-encoding
XX DNA to which CDRs were to be transplanted. DNAs given in
XX CC AAQ63448-53 were synthesised and ligated in order to obtain
XX a DNA, hKM796L (AAQ77823).
XX
XX Sequence 45 BP; 9 A; 14 C; 9 G; 13 T; 0 other;

Query Match 59.1%; Score 13.6; DB 15; Length 45;
Best Local Similarity 80.0%; Pred. No. 3e+03;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 accaggcgtctcgtggccca 20
DB 25 acctggcttctggtgcca 44

RESULT 14
AAAX99493
ID AAAX99493 standard; DNA; 45 BP.
XX
XX AAAX99493;
XX
XX 04-NOV-1999 (first entry)
XX
XX Synthetic DNA for production of hKM796L, from REI.
XX nucleotide; primer; immunoglobulin; light chain; plasmid;
XX REI; ds.
XX
XX Synthetic.
XX Homo sapiens.
XX
XX US5939532-A.
XX
XX 17-AUG-1999.
XX
XX 07-JUN-1995; 95US-0483528.
XX
XX 07-JUN-1995; 95US-0483528.
XX
XX 07-SEP-1993; 93US-0116778.
XX
XX (KYOW ) KYOWA HAKKO KOGYO KK.
```

XX Hanai N, Hasegawa M, Koike M, Kuwana Y, Nakamura K;
PI Shitara K;
XX WPI; 1999-468416/39.
XX Chimeric human antibody expression vectors
PT Chimeric human antibody expression vectors
XX Example 2; Column 105-107; 188pp; English.
XX This sequence can be used with sequences AAX99490 to AAX99495 to replace
CC part of the REI DNA, which is acting as a substitute immunoglobulin
CC heavy chain. The resulting DNA encodes for the human KM796 light chain.
CC The chimeric human antibodies are useful in the treatment of
CC cancer, especially that which is of neural ectodermal origin.
CC In contrast to prior art constructs based on mouse monoclonal
CC antibodies, the chimeric human antibodies do not cause
CC anti-mouse immunoglobulin production.
CC The chimeric human antibodies have a prolonged half-life and a
CC reduced frequency of adverse effects when compared to mouse monoclonal
CC antibodies.
XX Sequence 45 BP; 9 A; 14 C; 9 G; 13 T; 0 other;
SQ

Query Match 59.1%; Score 13.6; DB 20; Length 45;
Best Local Similarity 80.0%; Pred. No. 3e+03;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 accaggcgctctcgtgggcca 20
||| ||| ||| ||| ||| |||
Db 25 acctggctctcgtgtgcca 44

RESULT 15
AAV32874/C
ID AAV32874 standard; cDNA; 27 BP.
XX
AC AAV32874;
XX
DT 09-NOV-1998 (first entry)
XX
DE Human Borna disease virus p40 DNA 5' PCR primer.
XX
KW BDV; infection; diagnosis; neuropsychiatric disorder; human;
KW PCR; primer; ss.
XX
OS Synthetic.
OS Borna disease virus.
XX
FN WO9830238-A1.
XX
PD 16-JUL-1998.
XX
PF 07-JAN-1998; 98WO-US00495.
XX
PR 07-JAN-1997; 97US-0779764.
XX
PA (SCRI) SCRIPPS RES INST.
XX
PI De La Torre JC;
XX
DR WPI; 1998-398802/34.
XX
XX New isolated human Borna disease nucleic acid(s) - which encode p24,
PT p16, p56, p40 and L polymerase catalytic domain polypeptide(s),
PT used to develop products for detection
XX
XX Example; Page 107; 207pp; English.
PS
XX This 5' primer is used with a 3' primer (see AAV32875) in the
CC PCR amplification of cDNA (see AAV32851-53) coding for the p40
CC polypeptide (see AAW49051-53) of human borna disease virus (BDV).
*..CC

CC The PCR product is suitable for incorporation into a baculovirus
CC expression system, and recombinant polypeptide can be produced in
CC Spodoptera frugiperda sf158 cells. Human BDV polypeptides,
CC polynucleotides and antibodies are used in claimed methods for
CC detecting human BDV or human BDV-like viral infection,
CC particularly in patients with neuropsychiatric disorders.
XX
SQ Sequence 27 BP; 6 A; 8 C; 8 G; 5 T; 0 other;

Query Match 58.3%; Score 13.4; DB 19; Length 27;
Best Local Similarity 73.9%; Pred. No. 3.7e+03;
Matches 17; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 accaggcgctctcgtgggcca 23
| ||| ||| ||| ||| |||
Db 23 ATCAGGCGCTCTCCGGGTGGCAT 1

Search completed: August 17, 2002, 23:28:35
Job time: 4115 sec

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GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: August 17, 2002, 22:16:15 ; Search time 45.56 Seconds
(without alignments)
124.003 Million cell updates/sec

Title: US-09-700-906A-3

Perfect score: 23

Sequence: 1 accagggtctctgtggccacat 23

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 383533 seqs, 122816752 residues

Total number of hits satisfying chosen parameters: 543772

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database : Issued_Patents_NA:*

1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:*

2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*

3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*

4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*

5: /cgn2_6/ptodata/1/ina/PTUS_COMB.seq:*

6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	14.6	63.5	23	1	US-08-624-545-66
2	14.2	61.7	30	4	US-09-242-690A-20
3	13.8	60.0	34	1	US-08-075-193-16
4	13.8	60.0	34	2	US-08-564-090A-16
5	13.8	60.0	34	5	PCT-US94-06698-16
6	13.6	59.1	20	1	US-08-306-546C-4
7	13.6	59.1	20	2	US-08-530-524A-4
8	13.6	59.1	45	1	US-07-946-421-36
9	13.6	59.1	45	1	US-08-459-310-6
10	13.6	59.1	45	2	US-08-116-778E-33
11	13.6	59.1	45	2	US-08-438-562-33
12	13.6	59.1	45	2	US-08-483-528B-33
13	13.6	59.1	45	3	US-08-673-799C-33
14	13.4	58.3	27	3	US-08-779-764A-60
15	13.4	58.3	42	2	US-08-930-274-5
16	12.6	54.8	27	1	US-08-343-785-13
17	12.6	54.8	27	2	US-08-462-221-13
18	12.6	54.8	27	3	US-08-946-458-13
19	12.6	54.8	34	2	US-08-483-528B-43
20	12.6	54.8	34	3	US-08-836-561-21
21	12.6	54.8	34	3	US-08-673-799C-43
22	12.6	54.8	35	1	US-08-458-067-36
23	12.6	54.8	35	5	PCT-US96-07795-36
24	12.6	54.8	35	5	PCT-US96-07796-36
25	12.4	53.9	25	4	US-09-306-405-61
26	12.4	53.9	29	1	US-08-712-241-15
27	12.4	53.9	37	4	US-09-600-747-4
28	12.4	53.9	39	12	US-08-289-803-3
29	12.4	53.9	39	12	US-08-289-803-2
30	12.4	53.9	42	4	US-09-289-803-1
31	12.2	53.0	17	1	US-08-373-124A-1649
32	12.2	53.0	17	1	US-08-435-628-1649
33	12.2	53.0	23	4	US-08-943-731-652
34	12.2	53.0	31	4	US-08-467-504-8
35	12.2	53.0	38	2	US-08-963-946-33
36	12.2	53.0	44	1	US-08-458-067-18
37	12.2	53.0	44	5	PCT-US96-07795-18
38	12.2	53.0	44	5	PCT-US96-07796-18
39	12	52.2	20	2	US-09-044-506A-7
40	12	52.2	22	3	US-08-905-359A-14
41	12	52.2	22	4	US-09-353-556-14
42	12	52.2	24	2	US-08-461-286-4
43	12	52.2	24	5	PCT-US92-02854-4
44	12	52.2	25	5	PCT-US92-02854-3
45	12	52.2	26	2	US-08-461-286-2
46	12	52.2	26	5	PCT-US92-02854-2
47	12	52.2	35	4	US-08-604-165-15
48	12	52.2	35	4	US-08-734-054B-15
49	12	52.2	36	4	US-08-604-165-14
50	12	52.2	36	4	US-08-734-054B-14
51	12	52.2	37	2	PCT-US95-02861-2
52	12	52.2	40	2	US-08-461-286-1
53	12	52.2	40	5	PCT-US92-02854-1
54	12	52.2	47	2	US-08-487-867-28
55	12	52.2	47	5	PCT-US96-09358-28
56	11.8	51.3	17	1	US-08-373-124A-1647
57	11.8	51.3	17	1	US-08-435-628-1647
58	11.8	51.3	31	3	US-08-870-529-18
59	11.8	51.3	39	4	US-09-475-316A-80
60	11.8	51.3	40	4	US-08-748-547-15
61	11.8	51.3	40	4	US-09-262-773-173
62	11.8	51.3	42	1	US-07-931-473B-178
63	11.8	51.3	42	1	US-08-714-131C-178
64	11.8	51.3	42	1	US-08-412-110-178
65	11.8	51.3	42	1	US-08-409-442A-178
66	11.8	51.3	42	2	US-08-469-609A-178
67	11.8	51.3	42	3	US-09-143-190-178
68	11.8	51.3	48	1	US-08-458-067-16
69	11.8	51.3	48	5	PCT-US96-03940-21
70	11.8	51.3	48	5	PCT-US96-03940-22
71	11.8	51.3	48	5	PCT-US96-03940-23
72	11.8	51.3	48	5	PCT-US96-03940-25
73	11.8	51.3	48	5	PCT-US96-07795-16
74	11.8	51.3	48	5	PCT-US96-07796-16
75	11.8	51.3	50	4	US-08-563-524A-12
76	11.8	51.3	50	4	US-08-563-524A-16
77	11.6	50.4	18	3	US-09-280-409-13
78	11.6	50.4	22	1	US-08-481-633B-4
79	11.6	50.4	22	1	US-08-480-493A-4
80	11.6	50.4	22	1	US-08-482-638A-4
81	11.6	50.4	26	4	US-08-943-731-281
82	11.6	50.4	28	2	US-08-859-998-688
83	11.6	50.4	28	4	US-09-225-928-688
84	11.6	50.4	30	2	US-08-630-182-5
85	11.6	50.4	31	1	US-08-066-281-1
86	11.6	50.4	33	1	US-08-438-639-63
87	11.6	50.4	33	1	US-07-813-338A-63
88	11.6	50.4	33	3	US-08-441-971-139
89	11.6	50.4	33	3	US-08-221-653-139
90	11.6	50.4	33	4	US-08-442-144A-139
91	11.6	50.4	33	4	US-08-441-970-139
92	11.6	50.4	37	1	US-08-608-584-2
93	11.6	50.4	38	1	US-08-208-886C-53
94	11.6	50.4	38	1	US-08-704-744-53
95	11.6	50.4	38	1	US-08-469-557-53
96	11.6	50.4	38	2	US-08-290-793B-53
97	11.6	50.4	38	3	US-08-284-516C-27
98	11.6	50.4	40	1	US-08-199-507B-27
99	11.6	50.4	40	1	US-08-441-828-27
100	11.6	50.4	40	1	US-08-441-828-27

101	11.6	50.4	50	2	US-08-488-402A-73	Sequence 73, Appl	174	11	47.8	32	4	US-08-897-333A-8	Sequence 8, Appl
102	11.6	50.4	50	2	US-08-484-552A-73	Sequence 73, Appl	175	11	47.8	33	1	US-08-438-639-38	Sequence 38, Appl
103	11.6	50.4	50	5	PCT-US96-09472-73	Sequence 73, Appl	176	11	47.8	33	1	US-07-813-338A-38	Sequence 38, Appl
c 104	11.4	49.6	17	3	US-09-985-090-21	Sequence 21, Appl	177	11	47.8	33	3	US-08-441-971-113	Sequence 113, Appl
c 105	11.4	49.6	17	3	US-09-165-543-22	Sequence 22, Appl	c 178	11	47.8	33	3	US-08-897-333A-7	Sequence 7, Appl
106	11.4	49.6	22	4	US-09-475-316A-81	Sequence 81, Appl	179	11	47.8	33	4	US-08-221-653-113	Sequence 113, Appl
107	11.4	49.6	22	4	US-08-881-189B-9	Sequence 9, Appl	180	11	47.8	33	4	US-08-442-144A-113	Sequence 113, Appl
c 108	11.4	49.6	26	2	US-08-859-998-1276	Sequence 1276, Ap	181	11	47.8	33	4	US-08-441-970-113	Sequence 113, Appl
c 109	11.4	49.6	26	4	US-09-225-928-1276	Sequence 1276, Ap	c 182	11	47.8	34	4	US-09-155-078-3	Sequence 3, Appl
c 110	11.4	49.6	27	1	US-08-712-241-16	Sequence 16, Appl	183	11	47.8	35	1	US-08-384-489-35	Sequence 35, Appl
111	11.4	49.6	27	3	US-08-513-974B-70	Sequence 70, Appl	184	11	47.8	35	1	US-08-384-489-37	Sequence 37, Appl
112	11.4	49.6	28	4	US-08-881-189B-19	Sequence 19, Appl	c 185	11	47.8	36	5	PCT-US94-09700-23	Sequence 23, Appl
c 113	11.4	49.6	30	1	US-08-483-743-5	Sequence 5, Appl	186	11	47.8	37	4	US-09-450-072-41	Sequence 41, Appl
c 114	11.4	49.6	30	1	US-08-483-743-6	Sequence 6, Appl	c 187	11	47.8	40	2	US-08-963-946-6	Sequence 6, Appl
c 115	11.4	49.6	30	1	US-08-474-624-5	Sequence 5, Appl	188	11	47.8	41	2	US-08-963-946-5	Sequence 5, Appl
116	11.4	49.6	30	3	US-08-474-624-6	Sequence 6, Appl	189	11	47.8	48	1	US-08-137-117D-81	Sequence 81, Appl
c 117	11.4	49.6	30	3	US-08-803-085-15	Sequence 15, Appl	190	11	47.8	48	1	US-08-436-717-81	Sequence 81, Appl
c 118	11.4	49.6	31	3	US-09-200-232-3	Sequence 3, Appl	191	10.8	47.0	20	1	US-07-940-242A-80	Sequence 80, Appl
119	11.4	49.6	31	3	US-09-219-932-6	Sequence 6, Appl	192	10.8	47.0	21	4	US-08-050-482A-7	Sequence 7, Appl
c 120	11.4	49.6	32	1	US-08-912-976-9	Sequence 9, Appl	c 193	10.8	47.0	24	2	US-08-851-135-10	Sequence 10, Appl
c 121	11.4	49.6	32	4	US-08-844-045C-6	Sequence 6, Appl	c 194	10.8	47.0	24	2	US-08-787-902A-4	Sequence 4, Appl
c 122	11.4	49.6	32	4	US-09-476-299-29	Sequence 29, Appl	c 195	10.8	47.0	24	4	US-09-344-700-14	Sequence 14, Appl
c 123	11.4	49.6	36	2	US-09-609-154-29	Sequence 29, Appl	c 196	10.8	47.0	24	4	US-09-450-072-25	Sequence 25, Appl
c 124	11.4	49.6	36	2	US-08-432-071B-9	Sequence 9, Appl	c 197	10.8	47.0	25	4	US-09-098-628-65	Sequence 65, Appl
c 125	11.4	49.6	36	4	US-09-275-850-156	Sequence 156, App	198	10.8	47.0	25	4	US-09-546-250-6	Sequence 6, Appl
c 126	11.4	49.6	36	5	PCT-US96-06075-5	Sequence 5, Appl	199	10.8	47.0	26	2	US-08-483-528B-42	Sequence 42, Appl
127	11.4	49.6	41	3	US-09-167-354-4	Sequence 4, Appl	c 200	10.8	47.0	26	2	US-08-859-998-376	Sequence 376, Appl
c 128	11.4	49.6	44	4	US-09-159-290-24	Sequence 24, Appl	c 201	10.8	47.0	26	3	US-08-836-561-20	Sequence 20, Appl
c 129	11.4	49.6	44	3	US-09-046-247-16	Sequence 16, Appl	c 202	10.8	47.0	26	3	US-08-673-799C-42	Sequence 42, Appl
c 130	11.2	48.7	18	2	US-08-486-369-50	Sequence 50, Appl	c 203	10.8	47.0	26	4	US-09-225-928-376	Sequence 376, Appl
c 131	11.2	48.7	18	2	US-08-857-946-23	Sequence 23, Appl	c 204	10.8	47.0	27	1	US-08-338-992B-7	Sequence 7, Appl
c 132	11.2	48.7	18	3	US-08-970-740-23	Sequence 23, Appl	c 205	10.8	47.0	27	5	PCT-US95-09057-7	Sequence 7, Appl
c 133	11.2	48.7	18	3	US-09-280-409-57	Sequence 57, Appl	c 206	10.8	47.0	28	1	US-08-292-081A-2	Sequence 2, Appl
c 134	11.2	48.7	18	3	US-09-280-409-92	Sequence 92, Appl	c 207	10.8	47.0	28	2	US-08-752-495-2	Sequence 2, Appl
c 135	11.2	48.7	22	1	US-08-531-747-8	Sequence 8, Appl	c 208	10.8	47.0	29	2	US-08-467-603-31	Sequence 31, Appl
136	11.2	48.7	22	1	US-08-531-749-8	Sequence 8, Appl	c 209	10.8	47.0	29	2	US-08-466-793-31	Sequence 31, Appl
137	11.2	48.7	22	1	US-08-781-432-8	Sequence 8, Appl	c 210	10.8	47.0	29	2	US-08-491-861A-31	Sequence 31, Appl
c 138	11.2	48.7	23	2	US-08-859-998-1247	Sequence 1247, Ap	c 211	10.8	47.0	30	1	US-07-832-905B-29	Sequence 29, Appl
c 139	11.2	48.7	23	4	US-09-225-928-1247	Sequence 1247, Ap	c 212	10.8	47.0	30	1	US-08-153-848-58	Sequence 58, Appl
140	11.2	48.7	24	4	US-09-067-626-6	Sequence 6, Appl	c 213	10.8	47.0	30	1	US-08-153-848-58	Sequence 58, Appl
141	11.2	48.7	25	4	US-09-672-609-34	Sequence 34, Appl	c 214	10.8	47.0	30	2	US-08-700-757-29	Sequence 29, Appl
142	11.2	48.7	25	4	US-08-841-483-11	Sequence 11, Appl	c 215	10.8	47.0	30	2	US-08-821-782-27	Sequence 27, Appl
143	11.2	48.7	31	4	US-09-382-911-11	Sequence 11, Appl	c 216	10.8	47.0	30	3	US-09-299-843A-58	Sequence 58, Appl
144	11.2	48.7	38	2	US-08-715-941-10	Sequence 10, Appl	c 217	10.8	47.0	30	3	US-09-299-843A-59	Sequence 59, Appl
145	11.2	48.7	39	1	US-08-199-507B-29	Sequence 29, Appl	c 218	10.8	47.0	30	3	US-09-084-120-8	Sequence 8, Appl
146	11.2	48.7	39	1	US-08-199-507B-51	Sequence 51, Appl	c 219	10.8	47.0	30	4	US-09-292-435A-27	Sequence 27, Appl
147	11.2	48.7	39	1	US-08-441-928-29	Sequence 29, Appl	c 220	10.8	47.0	30	4	US-09-088-337B-58	Sequence 58, Appl
148	11.2	48.7	39	1	US-08-441-928-51	Sequence 51, Appl	c 221	10.8	47.0	30	4	US-09-088-337B-59	Sequence 59, Appl
149	11.2	48.7	40	1	US-08-199-507B-45	Sequence 45, Appl	c 222	10.8	47.0	30	5	PCT-US93-11153-58	Sequence 58, Appl
150	11.2	48.7	40	1	US-08-199-507B-50	Sequence 50, Appl	c 223	10.8	47.0	30	5	PCT-US93-11153-59	Sequence 59, Appl
151	11.2	48.7	40	1	US-08-441-928-45	Sequence 45, Appl	c 224	10.8	47.0	31	1	US-08-114-859-2	Sequence 2, Appl
152	11.2	48.7	40	1	US-08-441-928-50	Sequence 50, Appl	c 225	10.8	47.0	31	2	US-08-858-623A-20	Sequence 20, Appl
153	11.2	48.7	43	3	US-08-874-825-48	Sequence 48, Appl	c 226	10.8	47.0	33	2	US-08-858-623A-9	Sequence 9, Appl
154	11.2	48.7	43	3	US-08-663-824-48	Sequence 48, Appl	c 227	10.8	47.0	35	3	US-09-178-089-2	Sequence 2, Appl
155	11.2	48.7	49	2	US-08-450-370A-2	Sequence 2, Appl	c 228	10.8	47.0	39	1	US-08-418-123A-20	Sequence 20, Appl
c 156	11	47.8	19	4	US-09-226-012-56	Sequence 56, Appl	c 229	10.8	47.0	39	2	US-08-938-858-10	Sequence 10, Appl
c 157	11	47.8	23	2	US-08-461-286-5	Sequence 5, Appl	c 230	10.8	47.0	39	3	US-08-963-927-10	Sequence 10, Appl
158	11	47.8	23	5	PCT-US92-02854-5	Sequence 5, Appl	c 231	10.8	47.0	39	4	US-09-481-810-10	Sequence 10, Appl
159	11	47.8	26	1	US-08-467-607-20	Sequence 20, Appl	c 232	10.8	47.0	40	1	US-08-458-067-17	Sequence 17, Appl
160	11	47.8	26	2	US-08-469-362-20	Sequence 20, Appl	c 233	10.8	47.0	40	4	US-09-171-945-129	Sequence 129, Appl
161	11	47.8	26	2	US-08-850-392-20	Sequence 20, Appl	c 234	10.8	47.0	40	5	PCT-US96-07795-17	Sequence 17, Appl
162	11	47.8	27	1	US-08-264-861A-9	Sequence 9, Appl	c 235	10.8	47.0	40	5	PCT-US96-07796-17	Sequence 17, Appl
163	11	47.8	27	1	US-08-478-039-29	Sequence 29, Appl	c 236	10.8	47.0	42	3	US-08-874-825-12	Sequence 12, Appl
164	11	47.8	27	1	US-08-149-099C-7	Sequence 7, Appl	c 237	10.8	47.0	42	3	US-08-663-824-12	Sequence 12, Appl
165	11	47.8	27	1	US-08-476-349A-29	Sequence 29, Appl	c 238	10.8	47.0	44	2	US-08-982-232-2	Sequence 2, Appl
166	11	47.8	27	1	US-08-476-275-10	Sequence 10, Appl	c 239	10.8	47.0	45	1	US-07-834-539A-59	Sequence 59, Appl
167	11	47.8	27	2	US-08-478-967A-7	Sequence 7, Appl	c 240	10.8	47.0	45	1	US-07-834-539A-60	Sequence 60, Appl
168	11	47.8	27	3	US-08-523-894-22	Sequence 22, Appl	c 241	10.8	47.0	45	1	US-08-053-131-107	Sequence 107, Appl
169	11	47.8	30	5	PCT-US95-07784-9	Sequence 9, Appl	c 242	10.8	47.0	45	1	US-08-053-131-108	Sequence 108, Appl
c 170	11	47.8	30	2	US-08-483-199-3	Sequence 3, Appl	c 243	10.8	47.0	45	1	US-08-645-641-107	Sequence 107, Appl
c 171	11	47.8	30	2	US-08-483-199-3	Sequence 3, Appl	c 244	10.8	47.0	45	1	US-08-645-641-108	Sequence 108, Appl
c 172	11	47.8	30	2	US-08-484-508-3	Sequence 3, Appl	c 245	10.8	47.0	45	1	US-07-853-408B-107	Sequence 107, Appl
c 173	11	47.8	31	3	US-09-123-764-5	Sequence 5, Appl	c 246	10.8	47.0	45	1	US-07-853-408B-108	Sequence 108, Appl

247	10.8	47.0	45	1	US-08-096-762-107	Sequence 107, App	320	10.6	46.1	27	1	US-08-035-634-13	Sequence 13, Appl
248	10.8	47.0	45	1	US-08-096-762-108	Sequence 108, App	321	10.6	46.1	27	1	US-08-682-073-5	Sequence 5, Appli
249	10.8	47.0	45	1	US-08-800-353-59	Sequence 59, Appl	322	10.6	46.1	27	1	US-08-487-037-6	Sequence 6, Appli
250	10.8	47.0	45	2	US-08-800-353-60	Sequence 60, Appl	c 323	10.6	46.1	27	2	US-09-254-325-8	Sequence 8, Appli
251	10.8	47.0	45	2	US-08-308-865-107	Sequence 107, App	324	10.6	46.1	32	2	US-08-737-271-2	Sequence 2, Appli
252	10.8	47.0	45	2	US-08-308-865-108	Sequence 108, App	325	10.6	46.1	32	3	US-09-058-555-2	Sequence 2, Appli
253	10.8	47.0	45	2	US-08-982-232-1	Sequence 1, Appli	326	10.6	46.1	33	3	US-08-470-124-64	Sequence 64, Appl
254	10.8	47.0	45	3	US-08-863-813A-56	Sequence 56, Appl	327	10.6	46.1	33	3	US-08-441-971-130	Sequence 130, App
255	10.8	47.0	45	4	US-09-042-353-300	Sequence 300, App	328	10.6	46.1	33	4	US-08-221-653-130	Sequence 130, App
256	10.8	47.0	45	4	US-09-042-353-301	Sequence 301, App	329	10.6	46.1	33	4	US-08-442-144A-130	Sequence 130, App
257	10.8	47.0	45	4	US-08-758-417A-148	Sequence 148, App	330	10.6	46.1	33	4	US-08-441-970-130	Sequence 130, App
258	10.8	47.0	45	4	US-08-758-417A-149	Sequence 149, App	331	10.6	46.1	35	1	US-08-912-976-26	Sequence 26, Appl
259	10.8	47.0	45	5	PCT-US92-06185-59	Sequence 59, Appl	332	10.6	46.1	36	1	US-08-608-584-1	Sequence 1, Appli
260	10.8	47.0	45	5	PCT-US92-06185-60	Sequence 60, Appl	333	10.6	46.1	36	2	US-08-889-909A-18	Sequence 18, Appl
261	10.8	47.0	45	5	PCT-US92-10983-107	Sequence 107, App	334	10.6	46.1	36	4	US-09-156-163A-18	Sequence 18, Appl
262	10.8	47.0	45	5	PCT-US92-10983-108	Sequence 108, App	c 335	10.6	46.1	37	4	US-07-875-790B-10	Sequence 10, Appl
263	10.8	47.0	46	1	US-08-403-762A-14	Sequence 14, Appl	336	10.6	46.1	38	1	US-08-182-114-3	Sequence 3, Appli
264	10.8	47.0	46	1	US-08-661-507-4	Sequence 4, Appli	337	10.6	46.1	39	1	US-08-608-584-4	Sequence 4, Appli
265	10.8	47.0	46	2	US-08-855-083-3	Sequence 3, Appli	338	10.6	46.1	39	1	US-08-682-218-24	Sequence 24, Appl
266	10.8	47.0	46	2	US-09-186-030-3	Sequence 3, Appli	339	10.6	46.1	40	1	US-08-682-218-23	Sequence 23, Appl
267	10.8	47.0	46	2	US-08-865-675-3	Sequence 3, Appli	340	10.6	46.1	40	3	US-08-949-770-3	Sequence 3, Appli
268	10.8	47.0	46	2	US-08-933-749-4	Sequence 4, Appli	341	10.6	46.1	40	3	US-08-875-944B-4	Sequence 4, Appli
269	10.8	47.0	46	2	US-09-237-510-3	Sequence 3, Appli	c 342	10.6	46.1	40	4	US-09-416-050A-33	Sequence 33, Appl
270	10.8	47.0	46	3	US-09-120-916-3	Sequence 3, Appli	343	10.6	46.1	40	4	US-09-416-050A-46	Sequence 46, Appl
271	10.8	47.0	46	3	US-08-964-020-7	Sequence 7, Appli	344	10.6	46.1	40	4	US-09-664-800-33	Sequence 33, Appl
272	10.8	47.0	46	3	US-09-235-583-4	Sequence 4, Appli	345	10.6	46.1	40	4	US-09-664-800-46	Sequence 46, Appl
273	10.8	47.0	46	4	US-09-599-164-4	Sequence 4, Appli	346	10.6	46.1	40	4	US-09-665-309-33	Sequence 33, Appl
274	10.8	47.0	48	1	US-08-292-081A-9	Sequence 9, Appli	347	10.6	46.1	40	4	US-09-665-309-46	Sequence 46, Appl
275	10.8	47.0	48	2	US-08-752-495-9	Sequence 9, Appli	348	10.6	46.1	40	4	US-09-661-569-33	Sequence 33, Appl
276	10.8	47.0	50	1	US-08-171-389-379	Sequence 379, App	c 349	10.6	46.1	40	4	US-09-661-569-46	Sequence 46, Appl
277	10.8	47.0	50	1	US-08-123-936-379	Sequence 379, App	350	10.6	46.1	42	4	US-09-290-577-32	Sequence 32, Appl
278	10.8	47.0	50	2	US-08-475-228A-379	Sequence 379, App	351	10.6	46.1	42	4	US-09-290-452-32	Sequence 32, Appl
279	10.8	47.0	50	3	US-08-482-080A-379	Sequence 379, App	352	10.6	46.1	42	4	US-09-290-338-32	Sequence 32, Appl
280	10.8	47.0	50	5	PCT-US93-12388-379	Sequence 379, App	353	10.6	46.1	43	4	US-09-439-897-40	Sequence 40, Appl
281	10.6	46.1	18	1	US-08-271-948A-55	Sequence 55, Appl	c 354	10.6	46.1	45	1	US-08-050-058B-29	Sequence 29, Appl
282	10.6	46.1	18	1	US-08-271-944A-55	Sequence 55, Appl	355	10.6	46.1	45	1	US-08-463-587A-29	Sequence 29, Appl
283	10.6	46.1	18	2	US-08-410-654B-32	Sequence 32, Appl	356	10.6	46.1	45	2	US-08-463-667A-33	Sequence 33, Appl
284	10.6	46.1	18	2	US-08-474-851-32	Sequence 32, Appl	c 357	10.6	46.1	45	2	US-08-441-871-85	Sequence 85, Appl
285	10.6	46.1	18	2	US-08-481-560-32	Sequence 32, Appl	358	10.6	46.1	45	3	US-08-923-854-29	Sequence 29, Appl
286	10.6	46.1	18	3	US-08-779-916A-55	Sequence 55, Appl	359	10.6	46.1	45	3	US-08-388-029A-96	Sequence 96, Appl
287	10.6	46.1	18	5	PCT-US95-08604-55	Sequence 55, Appl	360	10.6	46.1	45	3	US-08-863-813A-59	Sequence 59, Appl
288	10.6	46.1	18	5	PCT-US95-08606-55	Sequence 55, Appl	c 361	10.6	46.1	45	4	US-08-918-148-63	Sequence 63, Appl
289	10.6	46.1	19	4	US-09-502-966-9	Sequence 59, Appl	362	10.6	46.1	45	6	5244792-15	Patent No. 5244792
290	10.6	46.1	20	1	US-07-940-242A-8	Sequence 8, Appli	363	10.6	46.1	46	1	US-08-171-389-144	Sequence 144, App
291	10.6	46.1	20	1	US-08-557-139-30	Sequence 30, Appl	364	10.6	46.1	46	1	US-08-123-936-144	Sequence 144, App
292	10.6	46.1	20	4	US-09-435-296-60	Sequence 60, Appl	365	10.6	46.1	46	2	US-08-475-228A-144	Sequence 144, App
293	10.6	46.1	20	4	US-09-490-692-59	Sequence 59, Appl	c 366	10.6	46.1	46	3	US-08-482-080A-144	Sequence 144, App
294	10.6	46.1	20	4	US-09-268-710-3	Sequence 3, Appli	367	10.6	46.1	46	5	PCT-US93-12388-144	Sequence 144, App
295	10.6	46.1	21	2	US-08-793-229-6	Sequence 6, Appli	368	10.6	46.1	47	1	US-08-293-086-7	Sequence 7, Appli
296	10.6	46.1	21	3	US-09-285-957-6	Sequence 6, Appli	369	10.6	46.1	47	1	US-08-244-993-7	Sequence 7, Appli
297	10.6	46.1	22	1	US-07-884-811-6	Sequence 6, Appli	370	10.6	46.1	47	2	US-08-861-306-7	Sequence 7, Appli
298	10.6	46.1	22	1	US-07-885-971-6	Sequence 6, Appli	c 371	10.6	46.1	47	2	US-08-468-037A-34	Sequence 34, Appl
299	10.6	46.1	22	1	US-08-087-783A-6	Sequence 6, Appli	372	10.6	46.1	47	2	US-08-471-973A-34	Sequence 34, Appl
300	10.6	46.1	22	1	US-08-194-088B-6	Sequence 6, Appli	c 373	10.6	46.1	47	2	US-08-465-880-15	Sequence 15, Appl
301	10.6	46.1	22	1	US-08-435-501-5	Sequence 5, Appli	374	10.6	46.1	47	3	US-09-035-357-34	Sequence 34, Appl
302	10.6	46.1	22	1	US-08-599-253-53	Sequence 53, Appl	c 375	10.6	46.1	47	3	US-09-016-520-16	Sequence 16, Appl
303	10.6	46.1	22	1	US-08-435-764-5	Sequence 5, Appli	376	10.6	46.1	47	3	US-09-144-611-7	Sequence 7, Appli
304	10.6	46.1	22	1	US-08-792-078-5	Sequence 5, Appli	c 377	10.6	46.1	47	4	US-09-130-973-16	Sequence 16, Appl
305	10.6	46.1	22	2	PCT-US93-04648-6	Sequence 6, Appli	378	10.6	46.1	47	4	US-09-477-902-16	Sequence 16, Appl
306	10.6	46.1	22	5	PCT-US93-04717-5	Sequence 5, Appli	c 379	10.6	46.1	47	4	US-09-502-966-13	Sequence 13, Appl
307	10.6	46.1	22	5	PCT-US96-06352-53	Sequence 53, Appl	380	10.6	46.1	47	4	US-09-453-514A-7	Sequence 7, Appli
308	10.6	46.1	22	5	PCT-US96-06583-53	Sequence 53, Appl	381	10.6	46.1	49	1	US-08-429-181-34	Sequence 34, Appl
309	10.6	46.1	22	5	US-08-343-785-15	Sequence 15, Appl	382	10.6	46.1	49	1	US-08-164-388-34	Sequence 34, Appl
310	10.6	46.1	23	1	US-08-462-221-15	Sequence 15, Appl	c 383	10.6	46.1	49	2	US-08-652-558-21	Sequence 21, Appl
311	10.6	46.1	23	2	US-08-793-229-5	Sequence 5, Appli	384	10.4	45.2	13	3	US-08-882-046-78	Sequence 78, Appl
312	10.6	46.1	23	3	US-09-285-957-5	Sequence 5, Appli	c 385	10.4	45.2	15	1	US-08-182-968A-179	Sequence 179, App
313	10.6	46.1	23	3	US-08-946-458-15	Sequence 15, Appl	386	10.4	45.2	15	2	US-08-774-306A-179	Sequence 179, App
314	10.6	46.1	23	3	US-08-343-785-14	Sequence 14, Appl	c 387	10.4	45.2	15	3	US-09-064-156A-179	Sequence 179, App
315	10.6	46.1	25	1	US-08-462-221-14	Sequence 14, Appl	388	10.4	45.2	15	4	US-09-180-437-147	Sequence 147, App
316	10.6	46.1	25	2	US-08-946-458-14	Sequence 14, Appl	c 389	10.4	45.2	18	1	US-08-458-568A-12	Sequence 12, Appl
317	10.6	46.1	25	2	US-08-946-458-14	Sequence 14, Appl	390	10.4	45.2	19	3	US-08-840-551-4	Sequence 4, Appli
318	10.6	46.1	26	3	US-08-648-272-20	Sequence 20, Appl	391	10.4	45.2	20	1	US-07-952-442-10	Sequence 10, Appl
319	10.6	46.1					392	10.4	45.2	20	1	US-08-269-766-10	Sequence 10, Appl

539	10.4	45.2	48	3	US-08-874-825-5	Sequence 5, Appl	612	10.2	44.3	24	3	US-08-976-255-33	Sequence 33, Appl
540	10.4	45.2	48	3	US-09-041-780-15	Sequence 15, Appl	613	10.2	44.3	24	4	US-08-475-470A-16	Sequence 16, Appl
541	10.4	45.2	48	3	US-08-335-844A-64	Sequence 64, Appl	614	10.2	44.3	24	4	US-09-225-928-695	Sequence 695, Appl
542	10.4	45.2	48	3	US-08-487-077A-9	Sequence 9, Appl	c 615	10.2	44.3	24	5	PCT-US95-0409A-13	Sequence 13, Appl
543	10.4	45.2	48	3	US-08-663-824-5	Sequence 5, Appl	c 616	10.2	44.3	24	5	PCT-US95-04228-37	Sequence 37, Appl
544	10.4	45.2	48	3	US-08-485-863A-9	Sequence 9, Appl	c 617	10.2	44.3	25	1	US-08-182-961B-14	Sequence 14, Appl
545	10.4	45.2	48	4	US-08-485-049D-9	Sequence 9, Appl	618	10.2	44.3	25	3	US-08-513-974B-1	Sequence 1, Appl
546	10.4	45.2	48	4	US-09-191-136-7	Sequence 7, Appl	619	10.2	44.3	25	4	US-08-776-971-29	Sequence 29, Appl
547	10.4	45.2	48	4	US-09-191-608-6	Sequence 6, Appl	620	10.2	44.3	25	4	US-09-007-678B-14	Sequence 14, Appl
548	10.4	45.2	48	4	US-09-264-693-3	Sequence 3, Appl	621	10.2	44.3	26	1	US-08-288-728-20	Sequence 20, Appl
549	10.4	45.2	48	4	US-09-178-115-9	Sequence 9, Appl	622	10.2	44.3	26	1	US-08-330-535A-29	Sequence 29, Appl
550	10.4	45.2	48	4	US-09-177-776-9	Sequence 9, Appl	623	10.2	44.3	26	1	US-08-688-145-13	Sequence 13, Appl
551	10.4	45.2	49	1	US-08-055-390-9	Sequence 9, Appl	624	10.2	44.3	26	2	US-08-838-844-29	Sequence 29, Appl
552	10.4	45.2	50	1	US-08-171-389-112	Sequence 112, App	c 625	10.2	44.3	27	1	US-07-988-194A-31	Sequence 31, Appl
553	10.4	45.2	50	1	US-08-171-389-138	Sequence 138, App	626	10.2	44.3	27	2	US-08-726-012B-17	Sequence 17, Appl
554	10.4	45.2	50	1	US-08-123-936-112	Sequence 112, App	c 627	10.2	44.3	27	4	US-09-253-396A-121	Sequence 121, App
555	10.4	45.2	50	1	US-08-123-936-138	Sequence 138, App	c 628	10.2	44.3	27	4	US-08-479-737-31	Sequence 31, Appl
556	10.4	45.2	50	2	US-08-475-228A-112	Sequence 112, App	c 629	10.2	44.3	28	1	US-08-394-033-3	Sequence 3, Appl
557	10.4	45.2	50	2	US-08-475-228A-138	Sequence 138, App	c 630	10.2	44.3	28	2	US-08-463-081B-19	Sequence 19, Appl
558	10.4	45.2	50	2	US-08-479-733A-5	Sequence 5, App	631	10.2	44.3	28	2	US-08-463-081B-20	Sequence 20, Appl
559	10.4	45.2	50	2	US-08-479-733A-7	Sequence 7, Appl	c 632	10.2	44.3	28	2	US-08-461-379A-19	Sequence 19, Appl
560	10.4	45.2	50	2	US-08-479-733A-12	Sequence 12, Appl	633	10.2	44.3	28	2	US-08-461-379A-20	Sequence 20, Appl
561	10.4	45.2	50	2	US-08-479-733A-16	Sequence 16, Appl	c 634	10.2	44.3	28	2	US-08-462-390B-19	Sequence 19, Appl
562	10.4	45.2	50	3	US-08-487-427-5	Sequence 5, App	635	10.2	44.3	28	2	US-08-462-390B-20	Sequence 20, Appl
563	10.4	45.2	50	3	US-08-487-427-7	Sequence 7, Appl	c 636	10.2	44.3	28	3	US-08-463-074B-19	Sequence 19, Appl
564	10.4	45.2	50	3	US-08-487-427-12	Sequence 12, App	637	10.2	44.3	28	3	US-08-463-074B-20	Sequence 20, Appl
565	10.4	45.2	50	3	US-08-487-427-16	Sequence 16, Appl	c 638	10.2	44.3	28	3	US-08-465-585C-19	Sequence 19, Appl
566	10.4	45.2	50	3	US-08-482-080A-112	Sequence 112, App	c 639	10.2	44.3	28	3	US-08-465-585C-20	Sequence 20, Appl
567	10.4	45.2	50	3	US-08-482-080A-138	Sequence 138, App	c 640	10.2	44.3	28	3	US-08-652-446-19	Sequence 19, Appl
568	10.4	45.2	50	3	US-08-479-727A-5	Sequence 5, Appl	641	10.2	44.3	28	3	US-08-652-446-20	Sequence 20, Appl
569	10.4	45.2	50	3	US-08-479-727A-7	Sequence 7, Appl	c 642	10.2	44.3	28	6	5256770-36	Patent No. 5256770
570	10.4	45.2	50	3	US-08-479-727A-12	Sequence 12, Appl	643	10.2	44.3	29	3	US-09-126-280-16	Sequence 16, Appl
571	10.4	45.2	50	3	US-08-479-727A-16	Sequence 16, Appl	644	10.2	44.3	29	4	US-09-449-437A-16	Sequence 16, Appl
572	10.4	45.2	50	3	US-08-482-369A-5	Sequence 5, Appl	c 645	10.2	44.3	30	2	US-08-845-161A-44	Sequence 44, Appl
573	10.4	45.2	50	3	US-08-482-369A-7	Sequence 7, Appl	c 646	10.2	44.3	30	2	US-08-860-882A-1	Sequence 1, Appl
574	10.4	45.2	50	3	US-08-482-369A-12	Sequence 12, Appl	c 647	10.2	44.3	30	2	US-08-860-882A-3	Sequence 3, Appl
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577	10.4	45.2	50	3	US-09-009-217-22	Sequence 22, App	650	10.2	44.3	30	3	US-08-810-324-44	Sequence 44, Appl
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c 841	10	43.5	20	4	US-09-362-230-20	Sequence 20, Appl	c 914	10	43.5	30	3	US-08-874-563-14	Sequence 14, Appl
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Query Match 60.0%; Score 13.8; DB 2; Length 34;

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: GENERAL INFORMATION:
: APPLICANT:  Friderici, Karen
: APPLICANT:  Jones, Margaret
: APPLICANT:  Chen, Hong
: APPLICANT:  Cavanagh, Kevin
: TITLE OF INVENTION:  Bovine Beta-Mannosidase Gene and Methods
: TITLE OF INVENTION:  of use
: NUMBER OF SEQUENCES:  28
: CORRESPONDENCE ADDRESS:
: ADDRESSEE:  Harms, Dickey & Pierce, P.L.C.

```

STREET: P.O. Box 828
CITY: Bloomfield Hills
STATE: Michigan
COUNTRY: USA
ZIP: 48303
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/306,546C
FILING DATE: September 15, 1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
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REGISTRATION NUMBER: 36,683
REFERENCE/DOCKET NUMBER: 6550-00003
TELEPHONE: (810)641-1600
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INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 base pairs
TYPE: nucleic acid
TOPOLOGY: linear
MOLECULE TYPE: primer
US-08-306-546C-4

Query Match 59.1%; Score 13.6; DB 1; Length 20;
Best Local Similarity 80.0%; Pred. No. 6.2e+02;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

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Db 20 AGGTGTCGTGTTAGCCACTT 1

RESULT 7
US-08-530-524A-4/C
Sequence 4, Application US/08530524A
Patent No. 5837836
GENERAL INFORMATION:
APPLICANT: Friderici, Karen
APPLICANT: Jones, Margaret
APPLICANT: Chen, Hong
APPLICANT: Cavanagh, Kevin
TITLE OF INVENTION: Bovine Beta-Mannosidase Gene and Methods
TITLE OF INVENTION: of use
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESSEE: Harness, Dickey & Pierce, P.L.C.
STREET: P.O. Box 828
CITY: Bloomfield Hills
STATE: Michigan
COUNTRY: USA
ZIP: 48303
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/530,524A
FILING DATE: September 19, 1995
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Smith, DeAnn F.
REGISTRATION NUMBER: 36,683
REFERENCE/DOCKET NUMBER: 6550-00003DVA
TELECOMMUNICATION INFORMATION:

TELEPHONE: (810)641-1600
TELEFAX: (810)641-0270
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 base pairs
TYPE: nucleic acid
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TOPOLOGY: linear
MOLECULE TYPE: primer
US-08-530-524A-4

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Best Local Similarity 80.0%; Pred. No. 6.2e+02;
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RESULT 8
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Sequence 36, Application US/07946421
Patent No. 5558864
GENERAL INFORMATION:
APPLICANT: Bendig, Mary M.
APPLICANT: Kettleborough, Catherine A.
APPLICANT: Saldanha, Jose
TITLE OF INVENTION: Humanized and Chimeric Monoclonal
TITLE OF INVENTION: Antibodies
NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
ADDRESSEE: Millen, White, Zelano & Branigan, P.C.
STREET: 2200 Clarendon Boulevard, Suite 1400
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ZIP: 22201
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/946,421
FILING DATE: 06-NOV-1992
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/EP92/00480
FILING DATE: 04-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 911933892
FILING DATE: 06-MAR-1991
ATTORNEY/AGENT INFORMATION:
NAME: Hamlet-King, Diana
REGISTRATION NUMBER: 33,302
REFERENCE/DOCKET NUMBER: Merck 1430
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-243-6333
TELEFAX: 703-243-6410
TELEX: 64191
INFORMATION FOR SEQ ID NO: 36:
SEQUENCE CHARACTERISTICS:
LENGTH: 45 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-07-946-421-36

Query Match 59.1%; Score 13.6; DB 1; Length 45;
Best Local Similarity 80.0%; Pred. No. 6.4e+02;

Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 accaggcgtctcgtggcca 20
||| ||| ||| ||| ||| |||
Db 23 ACCTGGCTTCTGGTGGCCA 42

RESULT 9

US-08-459-310-6/c
; Sequence 6, Application US/08459310
; Patent No. 5645817
; GENERAL INFORMATION:
; APPLICANT: Seemann, Gerhard
; APPLICANT: Bosslet, Klaus
; TITLE OF INVENTION: Granulocyte-Binding Antibody Constructs,
; TITLE OF INVENTION: Their Preparation and Use
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
; STREET: 1300 I Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005

COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/459,310
; FILING DATE:
; CLASSIFICATION: 424

PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/100,963
; FILING DATE: 03-AUG-1993
; APPLICATION NUMBER: DE P 422 58 53.7
; FILING DATE: 05-AUG-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Wadler, Linda A.
; REGISTRATION NUMBER: 33,218
; REFERENCE/DOCKET NUMBER: 02481.1317-00000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-408-4000
; TELEFAX: 202-408-4400

INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 45 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-459-310-6

Query Match 59.1%; Score 13.6; DB 1; Length 45;
Best Local Similarity 80.0%; Pred. No. 6.4e+02;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 accaggcgtctcgtggcca 20
||| ||| ||| ||| ||| |||
Db 23 ACCTGGCTTCTGGTGGCCA 4

RESULT 10

US-08-116-778E-33
; Sequence 33, Application US/08116778E
; Patent No. 5830470
; GENERAL INFORMATION:
; APPLICANT: NAKAMURA, KAZUYASU
; APPLICANT: KOIKE, MASAMICHI
; APPLICANT: SHITARA, KENYA

APPLICANT: HANAI, NOBUO
APPLICANT: KUWANA, YOSHIHISA
APPLICANT: HASEGAWA, MAMORU
TITLE OF INVENTION: HUMANIZED ANTIBODIES
NUMBER OF SEQUENCES: 49
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON & VANDERHYE P.C.
STREET: 1100 NORTH GLEBE ROAD
CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: U.S.A.
ZIP: 22201-4714
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/116,778E
FILING DATE: 07-SEP-93
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: WILSON, MARY J.
REGISTRATION NUMBER: 32,955
REFERENCE/DOCKET NUMBER: 249-59
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)816-4000
TELEFAX: (703)816-4100
INFORMATION FOR SEQ ID NO: 33:
SEQUENCE CHARACTERISTICS:
LENGTH: 45 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid, synthetic DNA
US-08-116-778E-33

Query Match 59.1%; Score 13.6; DB 2; Length 45;
Best Local Similarity 80.0%; Pred. No. 6.4e+02;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 accaggcgtctcgtggcca 20
||| ||| ||| ||| ||| |||
Db 25 ACCTGGCTTCTGGTGGCCA 44

RESULT 11

US-08-438-562-33
; Sequence 33, Application US/08438562
; Patent No. 5874255
; GENERAL INFORMATION:
; APPLICANT: NAKAMURA, KAZUYASU
; APPLICANT: KOIKE, MASAMICHI
; APPLICANT: SHITARA, KENYA
; APPLICANT: HANAI, NOBUO
; APPLICANT: KUWANA, YOSHIHISA
; APPLICANT: HASEGAWA, MAMORU
TITLE OF INVENTION: HUMANIZED ANTIBODIES
NUMBER OF SEQUENCES: 49
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON & VANDERHYE P.C.
STREET: 1100 NORTH GLEBE ROAD
CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: U.S.A.
ZIP: 22201-4714
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/438,562
FILING DATE: 10-MAY-95
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/116,778
FILING DATE: 07-SEP-93
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: WILSON, MARY J.
REGISTRATION NUMBER: 32,955
REFERENCE/DOCKET NUMBER: 249-76
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)816-4000
TELEFAX: (703)816-4100
INFORMATION FOR SEQ ID NO: 33:
SEQUENCE CHARACTERISTICS:
LENGTH: 45 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid, synthetic DNA
US-08-438-562-33

Query Match 59.1%; Score 13.6; DB 2; Length 45;
Best Local Similarity 80.0%; Pred. No. 6.4e+02;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 accaggcgtctcgtgggcca 20
| | | | | | | | | | | | | | | | | | | | | |
Db 25 ACCTGGCTTCTGGTGTGCCA 44

RESULT 12
US-08-483-528B-33
Sequence 33, Application US/08483528B
Patent No. 5939532
GENERAL INFORMATION:
APPLICANT: NAKAMURA, KAZUYASU
APPLICANT: KOIKE, MASAMICHI
APPLICANT: SHITARA, KENYA
APPLICANT: HANAI, NOBUO
APPLICANT: KUWANA, YOSHIHISA
APPLICANT: HASEGAWA, MAMORU
TITLE OF INVENTION: HUMANIZED ANTIBODIES
NUMBER OF SEQUENCES: 103
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON & VANDERHVE P.C.
STREET: 1100 NORTH GLEBE ROAD
CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: U.S.A.
ZIP: 22201-4714
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/483,528B
FILING DATE: 07-JUN-95
CLASSIFICATION: 536
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)816-4000
TELEFAX: (703)816-4100
INFORMATION FOR SEQ ID NO: 33:
SEQUENCE CHARACTERISTICS:
LENGTH: 45 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid, synthetic DNA
US-08-483-528B-33

Query Match 59.1%; Score 13.6; DB 2; Length 45;
Best Local Similarity 80.0%; Pred. No. 6.4e+02;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 accaggcgtctcgtgggcca 20
| | | | | | | | | | | | | | | | | | | | | |
Db 25 ACCTGGCTTCTGGTGTGCCA 44

RESULT 13
US-08-673-799C-33
Sequence 33, Application US/08673799C
Patent No. 6042828
GENERAL INFORMATION:
APPLICANT: NAKAMURA, KAZUYASU
APPLICANT: KOIKE, MASAMICHI
APPLICANT: SHITARA, KENYA
APPLICANT: HANAI, NOBUO
APPLICANT: KUWANA, YOSHIHISA
APPLICANT: HASEGAWA, MAMORU
TITLE OF INVENTION: HUMANIZED ANTIBODIES
NUMBER OF SEQUENCES: 104
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON & VANDERHVE P.C.
STREET: 1100 NORTH GLEBE ROAD
CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: U.S.A.
ZIP: 22201-4714
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/673,799C
FILING DATE: 27-JUN-96
CLASSIFICATION: 536
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)816-4000
TELEFAX: (703)816-4100
INFORMATION FOR SEQ ID NO: 33:
SEQUENCE CHARACTERISTICS:
LENGTH: 45 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid, synthetic DNA
US-08-673-799C-33

Query Match 59.1%; Score 13.6; DB 3; Length 45;
Best Local Similarity 80.0%; Pred. No. 6.4e+02;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 accaggcgtctcgtgggcca 20
| | | | | | | | | | | | | | | | | | | | | |
Db 25 ACCTGGCTTCTGGTGTGCCA 44

RESULT 14
US-08-779-764A-60/c
Sequence 60, Application US/08779764A
Patent No. 6057094
GENERAL INFORMATION:
APPLICANT: de la Torre, Juan C.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR SCREENING
OF HUMAN BORNA DISEASE VIRUS
NUMBER OF SEQUENCES: 65
CORRESPONDENCE ADDRESS:
ADDRESSEE: THE SCRIPPS RESEARCH INSTITUTE

STREET: 10550 No. 6057094th Torrey Pines Road, TPC-8
CITY: La Jolla
STATE: California
COUNTRY: United States
ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/779,764A
FILING DATE: 16-DEC-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Fitting, Thomas
REGISTRATION NUMBER: 34,163
REFERENCE/DOCKET NUMBER: TSRI 465.0
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 784-2937
TELEFAX: (619) 784-9399
INFORMATION FOR SEQ ID NO: 60:
SEQUENCE CHARACTERISTICS:
LENGTH: 27 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-779-764A-60

Query Match 58.3%; Score 13.4; DB 3; Length 27;
Best Local Similarity 73.9%; Pred. No. 7.8e+02;
Matches 17; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 accagggtctcgtgggccacat 23
| ||||| |||| ||||
Db 23 ATCAGGCGTCTCCGGGTGGCAT 1

RESULT 15

US-08-930-274-5
Sequence 5, Application US/08930274
Patent No. 5932441
GENERAL INFORMATION:
APPLICANT:
APPLICANT:
APPLICANT:
TITLE OF INVENTION: VECTORS FOR DIFFERENTIAL EXPRESSION
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wenderoth, Lind & Ponack, L.L.P.
STREET: 2033 K Street, N.W., Suite 800
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20006
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/930,274
FILING DATE: September 29, 1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 95302196.1
FILING DATE: 31-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB 96/00765

FILING DATE: 29-MAR-1996
ATTORNEY/AGENT INFORMATION:
NAME: Warren M. Cheek, Jr.
REGISTRATION NUMBER: 33,367
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-721-8200
TELEFAX: 202-721-8250
TELEX:
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 42 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "synthetic primer"
US-08-930-274-5

Query Match 58.3%; Score 13.4; DB 2; Length 42;
Best Local Similarity 73.9%; Pred. No. 7.9e+02;
Matches 17; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 accagggtctcgtgggccacat 23
| ||||| |||| ||||
Db 9 AGCATGCATCTAGAGGGCCGCAT 31

Search completed: August 17, 2002, 23:24:34
Job time: 4099 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 17, 2002, 21:27:35 ; Search time 1607.6 Seconds
(without alignments)
193.101 Million cell updates/sec

Title: US-09-700-906A-3
Perfect score: 23
Sequence: 1 accaggcgtctctgggccacat 23

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 13736207 seqs, 6748477542 residues

Total number of hits satisfying chosen parameters: 89578

Minimum DB seq length: 0
Maximum DB seq length: 50

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database :

- EST:*
- 1: em_estba:*
 - 2: em_esthum:*
 - 3: em_estin:*
 - 4: em_estmu:*
 - 5: em_estov:*
 - 6: em_estpl:*
 - 7: em_estro:*
 - 8: em_htc:*
 - 9: gb_est1:*
 - 10: gb_est2:*
 - 11: gb_htc:*
 - 12: gb_gss:*
 - 13: em_gss_hum:*
 - 14: em_gss_inv:*
 - 15: em_gss_pln:*
 - 16: em_gss_vrt:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	14.4	62.6	32	10	BG545479
2	14	60.9	50	9	AU106915
3	13.6	59.1	34	9	AU097023
C 4	13.2	57.4	34	9	AU537615
5	13.2	57.4	50	9	AU102952
C 6	13.2	57.4	50	9	AU106296
C 7	13	56.5	44	10	T64778
8	12.6	54.8	32	10	BM395935
9	12.6	54.8	43	9	AI685223
10	12.6	54.8	50	9	AU106914
11	12.6	54.8	50	9	AU106917
12	12.6	54.8	50	9	AU106918
13	12.6	54.8	50	9	AU106920
C 14	12.6	54.8	50	12	AZ789608
15	12.4	53.9	38	12	AZ309417
16	12.4	53.9	50	9	AU102221
17	12.4	53.9	50	10	BE547372

C 91	10.8	47.0	25	12	AZ782142	AZ782142 2M0022H10	164	10.4	45.2	46	12	AZ445453
C 92	10.8	47.0	34	12	TA102C06P	AL462338 T. brucei	C 165	10.4	45.2	48	9	AA934014
C 93	10.8	47.0	37	9	AA149901	AA149901 zo02f05.r	166	10.4	45.2	48	10	BE622110
C 94	10.8	47.0	37	10	W05633	W05633 za90d08.r1	167	10.4	45.2	49	9	AA045123
C 95	10.8	47.0	40	9	AA933656	AA933656 om56d08.s	C 168	10.4	45.2	50	9	AU102253
C 96	10.8	47.0	43	9	AI679845	AI679845 tu66e07.x	C 169	10.4	45.2	50	9	AU102469
C 97	10.8	47.0	44	12	AZ441861	AZ441861 IM0234D18	C 170	10.4	45.2	50	9	AU102478
C 98	10.8	47.0	45	10	BI388653	BI388653 EST-CD34N	C 171	10.4	45.2	50	9	AU104209
100	10.8	47.0	46	10	Z19605	Z19605 HSA00AAH P	172	10.4	45.2	50	9	AU104425
C 101	10.8	47.0	48	9	AI313698	AI313698 EST010 Mo	173	10.4	45.2	50	9	AU105619
C 102	10.8	47.0	49	9	AA948716	AA948716 Oq45h05.s	174	10.4	45.2	50	9	AU105922
C 103	10.8	47.0	49	9	AA975152	AA975152 om99c07.s	C 175	10.4	45.2	50	9	AU107936
104	10.8	47.0	50	9	AU102888	AU102888	176	10.2	44.3	26	12	AZ436027
105	10.8	47.0	50	9	AU103357	AU103357	177	10.2	44.3	29	12	TA71H09Q
106	10.8	47.0	50	9	AU103358	AU103358	C 178	10.2	44.3	30	10	BE727670
107	10.8	47.0	50	9	AU103359	AU103359	179	10.2	44.3	31	12	AZ432033
C 108	10.8	47.0	50	9	AU103361	AU103361	180	10.2	44.3	32	12	AZ597602
C 109	10.8	47.0	50	9	AU104872	AU104872	181	10.2	44.3	34	9	AA747497
C 110	10.8	47.0	50	9	AU104878	AU104878	182	10.2	44.3	34	9	AA887400
C 111	10.8	47.0	50	9	AU104879	AU104879	183	10.2	44.3	34	9	AI552428
C 112	10.8	47.0	50	9	AU104893	AU104893	C 184	10.2	44.3	34	9	AA221932
C 113	10.8	47.0	50	9	AU104917	AU104917	185	10.2	44.3	34	10	BF973182
C 114	10.8	47.0	50	9	AU105960	AU105960	C 186	10.2	44.3	34	12	TA80A07Q
C 115	10.6	46.1	50	9	AU106905	AU106905	C 187	10.2	44.3	35	12	AZ780177
C 116	10.6	46.1	25	9	AI608697	AI608697 tw26b02.x	C 188	10.2	44.3	37	10	BG390448
C 117	10.6	46.1	31	9	AA443732	AA443732 zw92d10.r	189	10.2	44.3	38	10	D19984
C 118	10.6	46.1	34	9	AI270065	AI270065 qt91f01.x	C 190	10.2	44.3	39	10	BJ063725
C 119	10.6	46.1	37	9	AA974682	AA974682 op29b04.s	C 191	10.2	44.3	40	9	AI1123628
120	10.6	46.1	37	10	BG976503	BG976503 602846752	C 192	10.2	44.3	40	10	R77790
121	10.6	46.1	37	10	W05633	W05633 za90d08.r1	C 193	10.2	44.3	41	12	AZ776137
C 122	10.6	46.1	40	9	AA687193	AA687193 nu26e05.s	C 194	10.2	44.3	42	12	AZ759249
C 123	10.6	46.1	40	12	BF340179	BF340179 602036555	C 195	10.2	44.3	42	12	TA130G07P
C 124	10.6	46.1	43	9	AZ651473	AZ651473 IM0522N07	196	10.2	44.3	43	9	AA074398
125	10.6	46.1	43	10	BI221669	BI221669 ub01h04.r	C 197	10.2	44.3	43	9	AI588855
C 126	10.6	46.1	47	9	AI789860	AI789860 602937102	198	10.2	44.3	45	12	AZ309694
127	10.6	46.1	50	9	AU103177	AU103177	C 199	10.2	44.3	45	9	AA982418
128	10.6	46.1	50	9	AU104426	AU104426	C 200	10.2	44.3	47	9	AW250812
129	10.6	46.1	50	9	AU104427	AU104427	201	10.2	44.3	47	12	AZ615317
130	10.6	46.1	50	9	AU104429	AU104429	C 202	10.2	44.3	47	12	TA100F09Q
131	10.6	46.1	50	9	AU104430	AU104430	C 203	10.2	44.3	49	9	AI195300
132	10.6	46.1	50	9	AU104946	AU104946	C 204	10.2	44.3	49	9	AI493938
C 133	10.6	46.1	50	9	AU104947	AU104947	205	10.2	44.3	49	10	BF203474
C 134	10.6	46.1	50	9	AU104966	AU104966	206	10.2	44.3	50	9	AI438119
C 135	10.6	46.1	50	9	AU104967	AU104967	C 207	10.2	44.3	50	9	AU102728
C 136	10.6	46.1	50	9	AU106297	AU106297	C 208	10.2	44.3	50	9	AU102729
137	10.6	46.1	50	9	AU106306	AU106306	C 209	10.2	44.3	50	9	AU102730
138	10.6	46.1	50	9	AU107261	AU107261	C 210	10.2	44.3	50	9	AU102732
139	10.6	46.1	50	9	AU107609	AU107609	211	10.2	44.3	50	9	AU102860
140	10.6	46.1	50	9	AU107610	AU107610	212	10.2	44.3	50	9	AU102972
C 141	10.6	46.1	50	9	AU107939	AU107939	C 213	10.2	44.3	50	9	AU103388
C 142	10.6	46.1	50	9	AW248108	AW248108 2819599.s	C 214	10.2	44.3	50	9	AU103970
143	10.6	46.1	50	10	T62585	T62585 yc04a07.r1	215	10.2	44.3	50	9	AU106605
C 144	10.4	45.2	21	12	AZ758704	AZ758704 IM0550A20	216	10.2	44.3	50	9	AU107339
C 145	10.4	45.2	24	12	AZ936903	AZ936903 2M0193E20	217	10.2	44.3	50	9	AU107830
C 146	10.4	45.2	28	12	AQ254833	AQ254833 EP212138	218	10.2	44.3	50	9	AU107832
C 147	10.4	45.2	31	10	BE387877	BE387877 601282104	219	10.2	44.3	50	9	AU107833
C 148	10.4	45.2	34	9	AI366127	AI366127 ao94f04.x	C 220	10.2	44.3	50	12	AZ800436
C 149	10.4	45.2	34	9	AI589397	AI589397 tr61h11.x	221	10.2	44.3	50	12	AZ917998
150	10.4	45.2	35	12	AZ654998	AZ654998 IM0529L12	222	10.2	44.3	50	12	BH624322
C 151	10.4	45.2	36	12	AZ828771	AZ828771 2M0106A02	C 223	10	43.5	23	12	TA338E01P
C 152	10.4	45.2	37	9	AI755616	AI755616 EtESTea38	224	10	43.5	25	10	BM399506
C 153	10.4	45.2	37	12	BH129921	BH129921 G-6C8.f M	C 225	10	43.5	26	12	AZ779432
C 154	10.4	45.2	38	10	BF144195	BF144195 601786804	C 226	10	43.5	29	10	BM3995762
155	10.4	45.2	39	12	AZ491251	AZ491251 IM0324N11	227	10	43.5	31	9	AA755576
C 156	10.4	45.2	40	12	TA96H01Q	TA96H01Q	228	10	43.5	31	9	AI651828
C 157	10.4	45.2	43	9	AW247061	AW247061 2822604.s	C 229	10	43.5	33	12	AZ304883
C 158	10.4	45.2	43	10	BI462985	BI462985 603204504	C 230	10	43.5	33	12	AZ805302
159	10.4	45.2	43	12	AZ514559	AZ514559 IM0361M10	231	10	43.5	34	10	BF579942
160	10.4	45.2	43	12	AZ658528	AZ658528 IM0535C14	232	10	43.5	34	12	AZ492829
C 161	10.4	45.2	46	9	AA019274	AA019274 ze56h10.s	233	10	43.5	34	12	AZ628045
162	10.4	45.2	46	9	AA878878	AA878878 of88h03.s	234	10	43.5	35	12	AZ621958
C 163	10.4	45.2	46	9	AI471447	AI471447 tml1f04.x	235	10	43.5	36	10	BG718554
							C 236	10	43.5	36	10	BG974649

c 237	10	43.5	36	10	BT109794	602901168	c 310	9.8	42.6	45	10	BM397811	5009-0-37
c 238	10	43.5	37	9	AA048244	mj27a04.r	311	9.8	42.6	46	9	AI744340	tt09q03.x
c 239	10	43.5	37	9	AI683252	to2e12.x	312	9.8	42.6	46	9	AI917121	ts052a12.x
c 240	10	43.5	37	10	N1581	zb24b07.s1	313	9.8	42.6	46	9	AA630952	nc76a01.s
c 241	10	43.5	38	9	AV833714	AV833714	314	9.8	42.6	46	10	B1651438	603298178
c 242	10	43.5	39	10	BF038837	601462043	c 315	9.8	42.6	46	12	AZ785255	2M0029106
c 243	10	43.5	40	10	H87341	YW16603.s1	c 316	9.8	42.6	47	12	AZ784478	2M0027K02
c 244	10	43.5	41	10	BJ077957	BJ077957	c 317	9.8	42.6	48	10	B1834201	603084104
c 245	10	43.5	41	10	BM399562	5009-0-59	c 318	9.8	42.6	48	12	AZ576659	AST-TD1.4
c 246	10	43.5	41	12	AZ990630	2M0274M23	c 319	9.8	42.6	48	12	AZ694184	AST-2HBG1
c 247	10	43.5	42	10	BG912536	602806638	c 320	9.8	42.6	49	10	D11784	HUMH01F06
c 248	10	43.5	42	10	B1656802	603281484	c 321	9.8	42.6	50	9	AU102606	AU102606
c 249	10	43.5	42	10	BF527907	602041058	c 322	9.8	42.6	50	9	AU103951	AU103951
c 250	10	43.5	43	9	AI367697	qy75d12.x	323	9.8	42.6	50	9	AU105396	AU105396
c 251	10	43.5	43	9	AI627640	ty81a12.x	324	9.8	42.6	50	9	AU105399	AU105399
c 252	10	43.5	43	10	W25159	zb59d02.r1	325	9.8	42.6	50	9	AU105400	AU105400
c 253	10	43.5	43	12	AZ447897	1M0245617	326	9.8	42.6	50	9	AU105402	AU105402
c 254	10	43.5	44	10	R78925	Y187607.s1	c 327	9.8	42.6	50	9	AU105696	AU105696
c 255	10	43.5	44	12	AQ090830	K16110-T7	c 328	9.8	42.6	50	9	AU105697	AU105697
c 256	10	43.5	45	12	AZ484607	AZ484607	329	9.8	42.6	50	9	AU105851	AU105851
c 257	10	43.5	46	9	AA671439	AA671439	c 330	9.8	42.6	50	9	AU105858	AU105858
c 258	10	43.5	46	9	AA537144	AA537144	c 331	9.8	42.6	50	9	AU105919	AU105919
c 259	10	43.5	46	12	AZ810685	2M0076624	c 332	9.8	42.6	50	9	AU106286	AU106286
c 260	10	43.5	47	12	AZ957982	2M0225L02	c 333	9.8	42.6	50	9	AU106354	AU106354
c 261	10	43.5	49	9	AA993146	qt77a10.s	334	9.8	42.6	50	9	AU107117	AU107117
c 262	10	43.5	49	9	AI192472	q65f04.x	335	9.8	42.6	50	9	AU107296	AU107296
c 263	10	43.5	49	10	T91886	YD54f05.s1	336	9.8	42.6	50	9	AU107297	AU107297
c 264	10	43.5	49	12	AZ613610	1M0442305	c 337	9.8	42.6	50	9	AU107432	AU107432
c 265	10	43.5	49	12	AZ830102	2M0109B11	c 338	9.8	42.6	50	9	AU108089	AU108089
c 266	10	43.5	50	9	AU102361	AU102361	339	9.8	42.6	50	10	B1651733	603298518
c 267	10	43.5	50	9	AU102877	AU102877	c 340	9.8	42.6	50	10	BE882523	601507265
c 268	10	43.5	50	9	AU103360	AU103360	c 341	9.8	42.6	50	12	AZ665355	1M0546F18
c 269	10	43.5	50	9	AU103481	AU103481	c 342	9.8	42.6	50	12	AZ675968	1M0563N12
c 270	10	43.5	50	9	AU104143	AU104143	c 343	9.6	41.7	22	9	AA954126	OG66A07.s
c 271	10	43.5	50	9	AU104144	AU104144	344	9.6	41.7	25	12	AZ511249	1M03556N10
c 272	10	43.5	50	9	AU104466	AU104466	345	9.6	41.7	25	12	AZ582580	1M0376N05
c 273	10	43.5	50	9	AU105104	AU105104	c 346	9.6	41.7	29	10	BM399121	5009-0-53
c 274	10	43.5	50	9	AU105106	AU105106	347	9.6	41.7	29	12	AZ508145	1M0350M09
c 275	10	43.5	50	9	AU105108	AU105108	348	9.6	41.7	31	12	AZ785133	2M0028J17
c 276	10	43.5	50	9	AU105124	AU105124	c 349	9.6	41.7	33	12	BH146188	BG02815-5
c 277	10	43.5	50	9	AU105919	AU105919	c 350	9.6	41.7	34	9	AA876855	ny47B08.s
c 278	10	43.5	50	9	AU107046	AU107046	c 351	9.6	41.7	35	12	AZ663930	1M0343N17
c 279	10	43.5	50	9	AU107603	AU107603	352	9.6	41.7	35	12	TA386F03Q	AL498283 T. brucei
c 280	10	43.5	50	10	BG033307	6032298562	353	9.6	41.7	36	10	B1861680	603389356
c 281	9.8	42.6	23	12	BI757063	BI757063	c 354	9.6	41.7	37	9	AI683252	tx02e12.x
c 282	9.8	42.6	23	12	TA130G06P	TA130G06P	c 355	9.6	41.7	37	9	AI721492	fc28A01.x
c 283	9.8	42.6	24	12	AZ826609	2M0102P18	c 356	9.6	41.7	37	10	BG976503	602846752
c 284	9.8	42.6	25	12	AZ872633	2M0186K01	c 357	9.6	41.7	37	10	BF211603	601812103
c 285	9.8	42.6	27	12	AZ422212	AZ422212	358	9.6	41.7	38	10	BF687876	602066947
c 286	9.8	42.6	31	9	AI287914	AI287914	c 359	9.6	41.7	40	9	AI188838	qd21f12.x
c 287	9.8	42.6	34	9	AI244815	q198B02.x	c 360	9.6	41.7	40	9	AI912669	we12a07.x
c 288	9.8	42.6	34	9	AI364208	q35h11.x	361	9.6	41.7	40	9	AA238160	mx16d10.r
c 289	9.8	42.6	34	9	AI584193	fb82a03.x	c 362	9.6	41.7	40	10	B1160469	602864532
c 290	9.8	42.6	36	10	BI731533	BI731533	c 363	9.6	41.7	40	12	AZ998247	2M0285P03
c 291	9.8	42.6	37	9	AI741717	wg22b07.x	364	9.6	41.7	41	9	AA665395	nu66A05.s
c 292	9.8	42.6	37	12	BH128739	G-5n16.f	365	9.6	41.7	41	12	AZ489214	1M0319G22
c 293	9.8	42.6	39	12	AZ774271	AZ774271	c 366	9.6	41.7	41	12	AZ598587	1M0413A04
c 294	9.8	42.6	39	12	AZ798493	AZ798493	c 367	9.6	41.7	41	12	AZ832185	2M0112L19
c 295	9.8	42.6	39	12	BH171128	BH171128	c 368	9.6	41.7	43	9	AA974942	on34h12.s
c 296	9.8	42.6	40	9	AI619480	AI619480	c 369	9.6	41.7	43	9	AI000393	ot06e05.s
c 297	9.8	42.6	40	9	AI628006	ty38g04.x	370	9.6	41.7	43	9	AI283782	qj75f08.x
c 298	9.8	42.6	40	9	AI720146	as78c02.x	371	9.6	41.7	43	9	AI507812	sa87e04.y
c 299	9.8	42.6	40	9	AA508464	AA508464	c 372	9.6	41.7	43	9	AI663481	uk33d07.y
c 300	9.8	42.6	40	12	TA274D05Q	TA274D05Q	c 373	9.6	41.7	43	12	AZ465400	1M0275K16
c 301	9.8	42.6	41	12	AZ950920	AZ950920	374	9.6	41.7	44	9	AV838294	AV838294
c 302	9.8	42.6	42	10	BI252223	BI252223	375	9.6	41.7	44	10	BG035308	602324932
c 303	9.8	42.6	42	10	BI252484	BI252484	c 376	9.6	41.7	44	10	BI918220	603183175
c 304	9.8	42.6	42	10	BF206391	BF206391	c 377	9.6	41.7	44	12	AQ02826	K071087-T
c 305	9.8	42.6	42	12	AZ380365	AZ380365	c 378	9.6	41.7	44	12	AZ444974	1M0240A01
c 306	9.8	42.6	42	12	AZ785539	AZ785539	c 379	9.6	41.7	45	10	BJ015280	BJ015280
c 307	9.8	42.6	43	9	AI802246	tj36e11.x	c 380	9.6	41.7	45	12	AZ832586	2M0113004
c 308	9.8	42.6	43	12	AZ345882	AI345882	c 381	9.6	41.7	45	12	TA321E02P	AL492361 T. brucei
c 309	9.8	42.6	44	10	BM396613	BM396613	382	9.6	41.7	46	9	AA743588	ny29d02.s

383	9.6	41.7	46	10	BI651438	BI651438 603298178	456	9.4	40.9	35	10	BM398446	BM398446 5009-0-45
c 384	9.6	41.7	48	10	W89968	W89968 mf64911.r1	457	9.4	40.9	35	12	AZ616370	AZ616370 1M0446H11
c 385	9.6	41.7	48	10	AL362060	AL362060 AL362060	c 458	9.4	40.9	36	10	BM400508	BM400508 5009-0-74
c 386	9.6	41.7	48	10	R77621	R77621 y176e12.r1	459	9.4	40.9	36	12	AZ487594	AZ487594 1M0317B21
c 387	9.6	41.7	48	12	AZ395292	AZ395292 1M0159C10	460	9.4	40.9	36	12	AZ800990	AZ800990 2M0059H15
c 388	9.6	41.7	49	9	AA724196	AA724196 a109d11.s	461	9.4	40.9	36	12	BH610366	BH610366 SALK_0087
c 389	9.6	41.7	49	9	AA828110	AA828110 od03c12.s	c 462	9.4	40.9	37	9	AI016514	AI016514 qt30h11.s
c 390	9.6	41.7	49	9	AA990502	AA990502 ua62906.s	463	9.4	40.9	37	9	AI188273	AI188273 qd11g10.x
391	9.6	41.7	49	9	AA995990	AA995990 os13h03.s	c 464	9.4	40.9	37	9	AI619702	AI619702 ty52a05.x
392	9.6	41.7	49	9	AA195871	AA195871 zp98g12.r	c 465	9.4	40.9	37	9	AI634572	AI634572 tz30a01.x
393	9.6	41.7	50	9	AA015340	AA015340 mh13c05.r	c 466	9.4	40.9	37	9	AI796585	AI796585 wh58b02.x
394	9.6	41.7	50	9	AO102598	AO102598 AO102598	467	9.4	40.9	37	10	BF130330	BF130330 601818394
395	9.6	41.7	50	9	AO102974	AO102974 AO102974	468	9.4	40.9	38	10	BM399387	BM399387 5009-0-57
396	9.6	41.7	50	9	AO102976	AO102976 AO102976	c 469	9.4	40.9	38	10	BF137365	BF137365 601780736
397	9.6	41.7	50	9	AO102978	AO102978 AO102978	c 470	9.4	40.9	39	10	BE729880	BE729880 601564916
398	9.6	41.7	50	9	AO102979	AO102979 AO102979	471	9.4	40.9	39	12	AZ771052	AZ771052 1M0572P22
399	9.6	41.7	50	9	AO103070	AO103070 AO103070	472	9.4	40.9	40	9	AI123084	AI123084 ok37f03.s
400	9.6	41.7	50	9	AO103432	AO103432 AO103432	c 473	9.4	40.9	40	9	AI800161	AI800161 tr23b08.x
401	9.6	41.7	50	9	AO104418	AO104418 AO104418	474	9.4	40.9	40	10	BG032379	BG032379 602301364
402	9.6	41.7	50	9	AO104428	AO104428 AO104428	475	9.4	40.9	40	10	BM397619	BM397619 5009-0-35
403	9.6	41.7	50	9	AO104681	AO104681 AO104681	c 476	9.4	40.9	40	10	R17398	R17398 y03d05.r1
404	9.6	41.7	50	9	AO104700	AO104700 AO104700	477	9.4	40.9	40	10	R55306	R55306 y177f05.s1
c 405	9.6	41.7	50	9	AO104732	AO104732 AO104732	c 478	9.4	40.9	40	10	T51935	T51935 yb28c09.s1
c 406	9.6	41.7	50	9	AO104896	AO104896 AO104896	c 479	9.4	40.9	40	12	AZ434256	AZ434256 1M0220L05
c 407	9.6	41.7	50	9	AO104899	AO104899 AO104899	480	9.4	40.9	40	12	BH628364	BH628364 1007079C1
408	9.6	41.7	50	9	AO105190	AO105190 AO105190	481	9.4	40.9	41	10	D74277	D74277 CELK079AXF
409	9.6	41.7	50	9	AO105191	AO105191 AO105191	c 482	9.4	40.9	41	12	AZ848135	AZ848135 2M0149A09
410	9.6	41.7	50	9	AO105192	AO105192 AO105192	483	9.4	40.9	41	12	AZ509020	AZ509020 2M0215L08
411	9.6	41.7	50	9	AO105193	AO105193 AO105193	484	9.4	40.9	42	9	AV838404	AV838404 AV838404
c 412	9.6	41.7	50	9	AO106834	AO106834 AO106834	c 485	9.4	40.9	42	9	AW250581	AW250581 2821639.5
c 413	9.6	41.7	50	9	AO106838	AO106838 AO106838	c 486	9.4	40.9	42	10	BG574349	BG574349 602536276
c 414	9.6	41.7	50	9	AO107016	AO107016 AO107016	c 487	9.4	40.9	42	10	H79257	H79257 yu48B02.s1
c 415	9.6	41.7	50	9	AO107176	AO107176 AO107176	c 488	9.4	40.9	42	10	T17558	T17558 mps v145 Th
c 416	9.6	41.7	50	9	AO107177	AO107177 AO107177	c 489	9.4	40.9	42	12	AZ628072	AZ628072 1M0480A05
417	9.6	41.7	50	9	AO107613	AO107613 AO107613	c 490	9.4	40.9	43	9	AA910920	AA910920 ok67h09.s
c 418	9.6	41.7	50	10	F37839	F37839 HSPD06947 H	491	9.4	40.9	43	9	AI088505	AI088505 qb17f07.x
c 419	9.6	41.7	50	12	AF087243	AF087243 AF087243	492	9.4	40.9	43	9	AA134736	AA134736 zm79g03.r
c 420	9.6	41.7	50	12	AZ247184	AZ247184 1M0209D02	c 493	9.4	40.9	43	9	AA134736	AA134736 zm79g03.r
c 421	9.6	41.7	50	12	AZ565607	AZ565607 211PVA09	c 494	9.4	40.9	43	9	AA1421857	AA1421857 tf55e11.x
c 422	9.6	41.7	50	12	AZ654289	AZ654289 1M0528E22	c 495	9.4	40.9	43	9	AA450033	AA450033 zx35a06.s
c 423	9.6	41.7	50	12	AZ817068	AZ817068 2M0086C07	c 496	9.4	40.9	43	12	AZ598505	AZ598505 1M0413B21
c 424	9.4	40.9	20	10	BM401265	BM401265 5009-0-85	497	9.4	40.9	44	10	H44436	H44436 y075b02.s1
c 425	9.4	40.9	21	12	AZ410517	AZ410517 1M0183W02	498	9.4	40.9	44	12	BH619995	BH619995 1007063H1
c 426	9.4	40.9	22	10	BM398778	BM398778 5009-0-5-	499	9.4	40.9	45	10	BM395809	BM395809 5009-0-12
c 427	9.4	40.9	23	12	AZ309209	AZ309209 1M0013F14	c 500	9.4	40.9	46	9	AA748313	AA748313 oa54b08.s
c 428	9.4	40.9	23	12	AZ448352	AZ448352 1M0246A06	c 501	9.4	40.9	46	9	AI355632	AI355632 qt76h04.x
c 429	9.4	40.9	24	10	BM400107	BM400107 5009-0-66	c 502	9.4	40.9	46	9	AI521423	AI521423 th60d09.x
c 430	9.4	40.9	24	12	AZ370614	AZ370614 1M0120L10	c 503	9.4	40.9	46	9	AA244435	AA244435 nc07f09.s
c 431	9.4	40.9	24	12	AZ825913	AZ825913 2M0101B22	c 504	9.4	40.9	46	10	R07615	R07615 ye98a03.s1
c 432	9.4	40.9	26	12	AZ377143	AZ377143 1M0131O17	c 505	9.4	40.9	46	12	AZ772856	AZ772856 1M0584M01
433	9.4	40.9	26	12	AZ600116	AZ600116 1M0416K16	c 506	9.4	40.9	46	12	BH169798	BH169798 SALK_0019
434	9.4	40.9	27	10	BM397484	BM397484 5009-0-33	c 507	9.4	40.9	46	12	BH624826	BH624826 1007111H0
c 435	9.4	40.9	28	9	AI376644	AI376644 te63b01.x	c 508	9.4	40.9	47	10	BG777442	BG777442 602664745
c 436	9.4	40.9	28	9	AI434082	AI434082 t141l03.x	c 509	9.4	40.9	47	12	TA107C12Q	TA107C12Q T. brucei
c 437	9.4	40.9	28	12	AZ618065	AZ618065 1M0449D11	c 510	9.4	40.9	48	10	BI906001	BI906001 603062308
c 438	9.4	40.9	28	12	AZ817375	AZ817375 2M0086N20	511	9.4	40.9	48	12	AZ796512	AZ796512 2M0052H18
439	9.4	40.9	29	12	TA380E12Q	TA380E12Q T. brucei	512	9.4	40.9	48	12	TA140E08P	TA140E08P T. brucei
c 440	9.4	40.9	29	12	AZ481100	AZ481100 1M0303D07	c 513	9.4	40.9	49	9	AA684136	AA684136 vm53b12.r
441	9.4	40.9	30	12	AZ591789	AZ591789 1M0402P06	c 514	9.4	40.9	49	9	AA907765	AA907765 om33h05.s
442	9.4	40.9	30	12	TA86E11P	TA86E11P T. brucei	c 515	9.4	40.9	49	9	AI200287	AI200287 qf86a10.x
443	9.4	40.9	31	2	HSM009800	AL044950 Homo sapi	516	9.4	40.9	49	9	AI416542	AI416542 sal10e02.y
444	9.4	40.9	31	9	AI032194	AI032194 zf96d04.s	517	9.4	40.9	49	9	AI758169	AI758169 ty70c07.x
445	9.4	40.9	31	10	N93307	N93307 zb96d02.s1	518	9.4	40.9	49	9	AI766723	AI766723 w103h12.x
446	9.4	40.9	31	12	AZ357525	AZ357525 1M0099B09	c 519	9.4	40.9	49	9	AA478678	AA478678 zw19g04.r
447	9.4	40.9	32	12	AZ601134	AZ601134 1M0419H13	c 520	9.4	40.9	49	10	BF970220	BF970220 602273453
448	9.4	40.9	33	10	BM396982	BM396982 5009-0-27	c 521	9.4	40.9	49	10	H22280	H22280 y136b03.r1
449	9.4	40.9	33	10	BM401378	BM401378 5009-0-9-	c 522	9.4	40.9	49	12	AQ073133	AQ073133 EP(3)3707
c 450	9.4	40.9	34	9	AI356596	AI356596 qu21e12.x	523	9.4	40.9	50	9	AO102220	AO102220 AO102220
451	9.4	40.9	34	9	AI610129	AI610129 tp13d02.x	c 524	9.4	40.9	50	9	AO102254	AO102254 AO102254
c 452	9.4	40.9	34	12	AZ763845	AZ763845 1M0559C04	525	9.4	40.9	50	9	AO102339	AO102339 AO102339
c 453	9.4	40.9	34	12	AZ800395	AZ800395 2M0058D23	c 526	9.4	40.9	50	9	AO102598	AO102598 AO102598
454	9.4	40.9	34	12	TA48H05Q	TA48H05Q T. brucei	c 527	9.4	40.9	50	9	AO102633	AO102633 AO102633
455	9.4	40.9	35	10	BI686449	BI686449 603312821	c 528	9.4	40.9	50	9	AO102635	AO102635 AO102635

529	9.4	40.9	50	9	AU102809	AU102809	AU102809	C 602	9.2	40.0	36	10	BF339163
C 530	9.4	40.9	50	9	AU102903	AU102903	AU102903	C 603	9.2	40.0	36	12	AZ613697
531	9.4	40.9	50	9	AU103003	AU103003	AU103003	C 604	9.2	40.0	37	12	AA007962
532	9.4	40.9	50	9	AU103167	AU103167	AU103167	C 605	9.2	40.0	37	9	AA112707
533	9.4	40.9	50	9	AU103169	AU103169	AU103169	C 606	9.2	40.0	37	9	AJ597737
534	9.4	40.9	50	9	AU103179	AU103179	AU103179	C 607	9.2	40.0	37	9	AI721492
C 535	9.4	40.9	50	9	AU103585	AU103585	AU103585	C 608	9.2	40.0	37	9	AY833316
C 536	9.4	40.9	50	9	AU103720	AU103720	AU103720	C 609	9.2	40.0	37	9	AA519406
C 537	9.4	40.9	50	9	AU103950	AU103950	AU103950	C 610	9.2	40.0	37	9	AA519406
C 538	9.4	40.9	50	9	AU103955	AU103955	AU103955	C 611	9.2	40.0	37	10	BF92074
539	9.4	40.9	50	9	AU103972	AU103972	AU103972	C 612	9.2	40.0	37	10	BG035903
C 540	9.4	40.9	50	9	AU104241	AU104241	AU104241	C 613	9.2	40.0	37	10	BG249841
C 541	9.4	40.9	50	9	AU105201	AU105201	AU105201	C 614	9.2	40.0	37	10	BI557903
C 542	9.4	40.9	50	9	AU105281	AU105281	AU105281	C 615	9.2	40.0	37	10	H45200
C 543	9.4	40.9	50	9	AU105660	AU105660	AU105660	C 616	9.2	40.0	37	12	AZ479159
544	9.4	40.9	50	9	AU105850	AU105850	AU105850	C 617	9.2	40.0	37	12	AZ592491
545	9.4	40.9	50	9	AU105887	AU105887	AU105887	C 618	9.2	40.0	37	12	AZ592491
C 546	9.4	40.9	50	9	AU106117	AU106117	AU106117	C 619	9.2	40.0	37	12	AZ666346
C 547	9.4	40.9	50	9	AU106138	AU106138	AU106138	C 620	9.2	40.0	37	12	AZ848874
C 548	9.4	40.9	50	9	AU106146	AU106146	AU106146	C 621	9.2	40.0	38	10	EG167790
C 549	9.4	40.9	50	9	AU106148	AU106148	AU106148	C 622	9.2	40.0	38	10	BG976935
C 550	9.4	40.9	50	9	AU106583	AU106583	AU106583	C 623	9.2	40.0	38	12	AZ312598
551	9.4	40.9	50	9	AU106598	AU106598	AU106598	C 624	9.2	40.0	39	10	BG921277
C 552	9.4	40.9	50	9	AU106742	AU106742	AU106742	C 625	9.2	40.0	39	10	BG968413
C 553	9.4	40.9	50	9	AU106840	AU106840	AU106840	C 626	9.2	40.0	39	12	AZ386752
C 554	9.4	40.9	50	9	AU107101	AU107101	AU107101	C 627	9.2	40.0	39	12	TAL13H06Q
C 555	9.4	40.9	50	9	AU107355	AU107355	AU107355	C 628	9.2	40.0	40	9	AJ1318261
C 556	9.4	40.9	50	9	AU107644	AU107644	AU107644	C 629	9.2	40.0	40	9	AJ421705
C 557	9.4	40.9	50	9	AU107847	AU107847	AU107847	C 630	9.2	40.0	40	9	AJ697005
C 558	9.4	40.9	50	9	AU107851	AU107851	AU107851	C 631	9.2	40.0	40	9	AJ749535
C 559	9.4	40.9	50	9	AU107879	AU107879	AU107879	C 632	9.2	40.0	40	9	AA589938
C 560	9.4	40.9	50	9	AU107881	AU107881	AU107881	C 633	9.2	40.0	40	10	BM397619
C 561	9.4	40.9	50	9	AU107903	AU107903	AU107903	C 634	9.2	40.0	40	10	H61510
C 562	9.4	40.9	50	9	AU107904	AU107904	AU107904	C 635	9.2	40.0	40	10	N98542
563	9.4	40.9	50	9	AU108003	AU108003	AU108003	C 636	9.2	40.0	40	12	AZ366373
C 564	9.4	40.9	50	9	AW631473	AW631473	AW631473	C 637	9.2	40.0	40	12	AZ438011
C 565	9.4	40.9	50	9	AW689710	AW689710	AW689710	C 638	9.2	40.0	40	12	AZ597065
C 566	9.4	40.9	50	12	AZ331635	AZ331635	AW0059008	C 639	9.2	40.0	40	12	AZ597065
C 567	9.4	40.9	50	12	AZ839200	AZ839200	2M0135A13	C 640	9.2	40.0	40	12	AZ987032
568	9.2	40.0	19	9	AI056541	AI056541	OY98C11.X	C 641	9.2	40.0	41	9	AV832542
569	9.2	40.0	21	12	AZ452159	AZ452159	1M0251D21	C 642	9.2	40.0	41	10	BG033041
C 570	9.2	40.0	22	9	AI660937	AI660937	Wf20B06.X	C 643	9.2	40.0	41	10	BF572131
571	9.2	40.0	25	12	TA90H05Q	AL459902	T. brucei	C 644	9.2	40.0	41	12	BF000491
C 572	9.2	40.0	26	12	AZ841913	AZ841913	2M0140T04	C 645	9.2	40.0	41	12	BH625029
573	9.2	40.0	27	12	AZ619590	AZ619590	1M0451H24	C 646	9.2	40.0	42	10	BG574349
574	9.2	40.0	27	12	AZ822698	AZ822698	2M0096109	C 647	9.2	40.0	42	12	AZ343437
C 575	9.2	40.0	27	12	AZ989590	AZ989590	2M0273D03	C 648	9.2	40.0	42	12	AZ586046
C 576	9.2	40.0	28	9	AI735009	AI735009	as44e04.X	C 649	9.2	40.0	42	12	AZ777657
577	9.2	40.0	28	10	H45597	H45597	Yn97e04.r1	C 650	9.2	40.0	42	12	AZ941495
578	9.2	40.0	28	12	AZ355807	AZ355807	1M0095G07	C 651	9.2	40.0	42	12	TA245F07Q
C 579	9.2	40.0	29	12	AZ479604	AZ479604	1M0300E21	C 652	9.2	40.0	43	9	AA037420
C 580	9.2	40.0	30	10	BJ080455	BJ080455	BJ080455	C 653	9.2	40.0	43	9	AA499553
C 581	9.2	40.0	30	10	C20895	C20895	HUMGS000496	C 654	9.2	40.0	43	10	BI830843
C 582	9.2	40.0	30	12	AZ774809	AZ774809	2M0004O05	C 655	9.2	40.0	43	10	BI830843
C 583	9.2	40.0	30	12	AZ854289	AZ854289	2M0157M17	C 656	9.2	40.0	44	10	BE378922
584	9.2	40.0	31	12	AZ372016	AZ372016	1M0123M09	C 657	9.2	40.0	44	12	AZ428590
C 585	9.2	40.0	31	12	AZ481183	AZ481183	1M0303G17	C 658	9.2	40.0	44	12	AZ487383
586	9.2	40.0	31	12	AZ807241	AZ807241	2M0069L24	C 659	9.2	40.0	44	12	AZ489056
C 587	9.2	40.0	32	10	RI0590	RI0590	Yf38C10.s1	C 660	9.2	40.0	44	12	AZ603654
C 588	9.2	40.0	32	12	AZ781627	AZ781627	2M0021F10	C 661	9.2	40.0	45	9	AA811409
C 589	9.2	40.0	34	9	AA936967	AA936967	OO65G02.s	C 662	9.2	40.0	45	10	BI556158
C 590	9.2	40.0	34	9	AI366127	AI366127	AO94f04.X	C 663	9.2	40.0	45	10	BI596480
591	9.2	40.0	34	9	AI739192	AI739192	W127g04.X	C 664	9.2	40.0	45	10	BI754711
592	9.2	40.0	34	9	AI799523	AI799523	tr49B05.X	C 665	9.2	40.0	45	12	AZ310900
593	9.2	40.0	34	10	BI143747	BI143747	602907208	C 666	9.2	40.0	45	12	AZ780685
C 594	9.2	40.0	34	10	BM397197	BM397197	5009-0-3-	C 667	9.2	40.0	46	9	AA869188
595	9.2	40.0	34	12	AZ784673	AZ784673	2M0027K22	C 668	9.2	40.0	46	9	AA914960
C 596	9.2	40.0	35	10	BF302658	BF302658	602032522	C 669	9.2	40.0	46	9	AJ544749
597	9.2	40.0	35	12	AZ467050	AZ467050	1M027BK12	C 670	9.2	40.0	46	9	AA151915
598	9.2	40.0	35	12	TA71H09P	AL457845	T. brucei	C 671	9.2	40.0	46	9	AA151915
C 599	9.2	40.0	36	10	BF969721	BF969721	602272124	C 672	9.2	40.0	46	10	T98810
C 600	9.2	40.0	36	10	BI255015	BI255015	602974538	C 673	9.2	40.0	46	10	W64843
C 601	9.2	40.0	36	10	BM396440	BM396440	5009-0-20	C 674	9.2	40.0	46	12	AZ487839

c 675	9.2	40.0	46	12	AZ487839	1M0317F14	748	9.2	40.0	50	9	AU105480	AU105480
c 676	9.2	40.0	47	10	BI110720	602895332	749	9.2	40.0	50	9	AU105679	AU105679
c 677	9.2	40.0	47	10	BJ001441	BJ001441	750	9.2	40.0	50	9	AU106620	AU106620
c 678	9.2	40.0	47	10	BE866303	601678950	751	9.2	40.0	50	9	AU106924	AU106924
c 679	9.2	40.0	47	12	AZ606685	1M0428A17	c 752	9.2	40.0	50	9	AU107547	AU107547
c 680	9.2	40.0	47	12	TA100F09Q	AL459357 T. brucei	c 753	9.2	40.0	50	9	AU108055	AU108055
c 681	9.2	40.0	47	12	TA130G01P	AL484118 T. brucei	c 754	9.2	40.0	50	9	AV676321	AV676321
c 682	9.2	40.0	47	12	TA324E04Q	AL490992 T. brucei	c 755	9.2	40.0	50	9	AW637027	AW637027
c 683	9.2	40.0	48	9	AA930873	AA930873 vz71e07.s	756	9.2	40.0	50	9	AA554519	AA554519
c 684	9.2	40.0	48	9	AI172854	AI172854 ucl0c07.r	c 757	9.2	40.0	50	10	BG938916	BG938916
c 685	9.2	40.0	48	9	AA386692	AA386692 vb55c05.r	c 758	9.2	40.0	50	10	BI665523	BI665523
c 686	9.2	40.0	48	9	AA484789	AA484789 ng09a11.s	c 759	9.2	40.0	50	10	D21029	D21029
c 687	9.2	40.0	48	10	BI697515	BI697515 603349071	c 760	9.2	40.0	50	10	BE311372	BE311372
c 688	9.2	40.0	48	10	BI829440	BI829440 603080458	c 761	9.2	40.0	50	12	AZ857216	AZ857216
c 689	9.2	40.0	48	12	AZ310125	AZ310125 1M0018M20	762	9.2	40.0	50	12	AZ938271	AZ938271
c 690	9.2	40.0	48	12	BH624836	BH624836 1007089A0	c 763	9.2	40.0	50	12	AZ309156	AZ309156
c 691	9.2	40.0	49	9	AA663894	AA663894 ae74c09.s	c 764	9.2	40.0	50	12	AZ309156	AZ309156
c 692	9.2	40.0	49	9	AA687445	AA687445 ns58906.s	c 765	9.2	40.0	50	12	BM396464	BM396464
c 693	9.2	40.0	49	9	AA711597	AA711597 vu24h02.r	c 766	9.2	40.0	50	12	BM400927	BM400927
c 694	9.2	40.0	49	9	AA902559	AA902559 oJ59b12.s	c 767	9.2	40.0	50	12	AZ336549	AZ336549
c 695	9.2	40.0	49	9	AI244893	AI244893 qJ98f06.x	768	9.2	40.0	50	12	BM397858	BM397858
c 696	9.2	40.0	49	9	AI308301	AI308301 ta90c10.x	769	9.2	40.0	50	12	AZ762598	AZ762598
c 697	9.2	40.0	49	9	AA541816	AA541816 n188d08.s	c 770	9.2	40.0	50	12	BM398868	BM398868
c 698	9.2	40.0	49	10	BG519127	BG519127 602578064	c 771	9.2	40.0	50	12	BM399175	BM399175
c 699	9.2	40.0	49	10	U44334	U44334 ENU44334 AS	772	9.2	40.0	50	9	AI565893	AI565893
c 700	9.2	40.0	49	10	BE376178	BE376178 601228534	c 773	9.2	40.0	50	12	AZ307137	AZ307137
c 701	9.2	40.0	49	12	AZ776457	AZ776457 2M0100004	774	9.2	40.0	50	12	AZ361612	AZ361612
c 702	9.2	40.0	49	12	AZ800315	AZ800315 2M0588G16	c 775	9.2	40.0	50	9	AA934268	AA934268
c 703	9.2	40.0	49	12	AZ803036	AZ803036 2M0063M11	c 776	9.2	40.0	50	9	AI560563	AI560563
c 704	9.2	40.0	50	9	AU102219	AU102219 AU102219	c 777	9.2	40.0	50	12	AZ480819	AZ480819
c 705	9.2	40.0	50	9	AU102279	AU102279 AU102279	c 778	9.2	40.0	50	12	AZ591905	AZ591905
c 706	9.2	40.0	50	9	AU102280	AU102280 AU102280	c 779	9.2	40.0	50	12	AZ829200	AZ829200
c 707	9.2	40.0	50	9	AU102532	AU102532 AU102532	780	9.2	40.0	50	12	AZ843789	AZ843789
c 708	9.2	40.0	50	9	AU102663	AU102663 AU102663	c 781	9.2	40.0	50	12	AG026067	AG026067
c 709	9.2	40.0	50	9	AU102822	AU102822 AU102822	c 782	9.2	40.0	50	10	BM398658	BM398658
c 710	9.2	40.0	50	9	AU102827	AU102827 AU102827	c 783	9.2	40.0	50	10	BM398658	BM398658
c 711	9.2	40.0	50	9	AU102861	AU102861 AU102861	784	9.2	40.0	50	10	BG819018	BG819018
c 712	9.2	40.0	50	9	AU103032	AU103032 AU103032	785	9.2	40.0	50	10	BM400355	BM400355
c 713	9.2	40.0	50	9	AU103033	AU103033 AU103033	c 786	9.2	40.0	50	10	BM400355	BM400355
c 714	9.2	40.0	50	9	AU103037	AU103037 AU103037	787	9.2	40.0	50	12	AZ394609	AZ394609
c 715	9.2	40.0	50	9	AU103038	AU103038 AU103038	c 788	9.2	40.0	50	12	AZ783888	AZ783888
c 716	9.2	40.0	50	9	AU103039	AU103039 AU103039	c 789	9.2	40.0	50	12	AZ792571	AZ792571
c 717	9.2	40.0	50	9	AU103040	AU103040 AU103040	790	9.2	40.0	50	12	AZ815328	AZ815328
c 718	9.2	40.0	50	9	AU104258	AU104258 AU104258	791	9.2	40.0	50	31	AI100097	AI100097
c 719	9.2	40.0	50	9	AU104263	AU104263 AU104263	c 792	9.2	40.0	50	31	AI688077	AI688077
c 720	9.2	40.0	50	9	AU104378	AU104378 AU104378	c 793	9.2	40.0	50	31	AI6767093	AI6767093
c 721	9.2	40.0	50	9	AU104390	AU104390 AU104390	794	9.2	40.0	50	31	BG920609	BG920609
c 722	9.2	40.0	50	9	AU104391	AU104391 AU104391	c 795	9.2	40.0	50	31	BM400833	BM400833
c 723	9.2	40.0	50	9	AU104394	AU104394 AU104394	796	9.2	40.0	50	10	BF235989	BF235989
c 724	9.2	40.0	50	9	AU104396	AU104396 AU104396	797	9.2	40.0	50	10	BF532788	BF532788
c 725	9.2	40.0	50	9	AU104397	AU104397 AU104397	c 798	9.2	40.0	50	12	AZ663905	AZ663905
c 726	9.2	40.0	50	9	AU104398	AU104398 AU104398	799	9.2	40.0	50	31	AZ809714	AZ809714
c 727	9.2	40.0	50	9	AU104399	AU104399 AU104399	c 800	9.2	40.0	50	31	AZ818116	AZ818116
c 728	9.2	40.0	50	9	AU104402	AU104402 AU104402	c 801	9.2	40.0	50	32	BM391939	BM391939
c 729	9.2	40.0	50	9	AU104405	AU104405 AU104405	802	9.2	40.0	50	32	BI094784	BI094784
c 730	9.2	40.0	50	9	AU104406	AU104406 AU104406	c 803	9.2	40.0	50	32	BM395935	BM395935
c 731	9.2	40.0	50	9	AU104407	AU104407 AU104407	c 804	9.2	40.0	50	33	BM396982	BM396982
c 732	9.2	40.0	50	9	AU104409	AU104409 AU104409	c 805	9.2	40.0	50	33	BM398846	BM398846
c 733	9.2	40.0	50	9	AU104412	AU104412 AU104412	806	9.2	40.0	50	33	BM398978	BM398978
c 734	9.2	40.0	50	9	AU104413	AU104413 AU104413	807	9.2	40.0	50	33	AZ311284	AZ311284
c 735	9.2	40.0	50	9	AU104414	AU104414 AU104414	c 808	9.2	40.0	50	33	AZ324178	AZ324178
c 736	9.2	40.0	50	9	AU104415	AU104415 AU104415	809	9.2	40.0	50	33	AZ759871	AZ759871
c 737	9.2	40.0	50	9	AU104416	AU104416 AU104416	c 810	9.2	40.0	50	34	AI241642	AI241642
c 738	9.2	40.0	50	9	AU104417	AU104417 AU104417	c 811	9.2	40.0	50	34	AI362411	AI362411
c 739	9.2	40.0	50	9	AU104419	AU104419 AU104419	812	9.2	40.0	50	34	AI368216	AI368216
c 740	9.2	40.0	50	9	AU104422	AU104422 AU104422	813	9.2	40.0	50	34	AI444187	AI444187
c 741	9.2	40.0	50	9	AU104423	AU104423 AU104423	814	9.2	40.0	50	34	AI584572	AI584572
c 742	9.2	40.0	50	9	AU104624	AU104624 AU104624	c 815	9.2	40.0	50	34	AA441877	AA441877
c 743	9.2	40.0	50	9	AU104698	AU104698 AU104698	816	9.2	40.0	50	34	BI094785	BI094785
c 744	9.2	40.0	50	9	AU104774	AU104774 AU104774	c 817	9.2	40.0	50	34	BI913027	BI913027
c 745	9.2	40.0	50	9	AU105027	AU105027 AU105027	818	9.2	40.0	50	34	BJ061523	BJ061523
c 746	9.2	40.0	50	9	AU105296	AU105296 AU105296	c 819	9.2	40.0	50	34	BJ063573	BJ063573
c 747	9.2	40.0	50	9	AU105428	AU105428 AU105428	c 820	9.2	40.0	50	34	BE546481	BE546481

821	9	39.1	34	12	AZ389322	AZ389322	1M0149C18	C 894	9	39.1	41	12	AZ990351	AZ990351	2M0274T01
822	9	39.1	34	12	AZ599278	AZ599278	1M0414G02	C 895	9	39.1	42	10	BM397149	BM397149	5009-0-29
823	9	39.1	34	12	AZ762551	AZ762551	1M0557K02	C 896	9	39.1	42	10	BE899162	BE899162	601681959
824	9	39.1	34	12	AZ763845	AZ763845	1M0559C04	C 897	9	39.1	42	12	AZ378074	AZ378074	1M0132K12
825	9	39.1	34	12	AZ814665	AZ814665	2M0082E02	C 898	9	39.1	43	9	AA754675	AA754675	vu20e01.r
C 826	9	39.1	34	12	AZ832199	AZ832199	2M0112P22	C 899	9	39.1	43	9	AI222474	AI222474	9912608.x
C 827	9	39.1	34	12	AZ875088	AZ875088	2M0189N23	C 900	9	39.1	43	9	AI569934	AI569934	tr57H08.x
C 828	9	39.1	34	12	BH000438	BH000438	2M0288I15	C 901	9	39.1	43	9	AI625677	AI625677	ty59b11.x
C 829	9	39.1	35	10	BF793800	BF793800	602254477	C 902	9	39.1	43	10	BF581977	BF581977	602781306
C 830	9	39.1	35	10	BF693679	BF693679	603342387	C 903	9	39.1	43	10	BF582059	BF582059	602099239
C 831	9	39.1	35	10	C01680	C01680	HUMGS000869	C 904	9	39.1	43	12	AZ378285	AZ378285	1M0133B01
C 832	9	39.1	35	10	BF7588	BF7588	YF61603.r1	C 905	9	39.1	43	12	AZ595428	AZ595428	2M0227P05
C 833	9	39.1	35	10	BF302658	BF302658	602032522	C 906	9	39.1	44	9	AL663346	AL663346	AL663346
C 834	9	39.1	35	12	AZ377416	AZ377416	1M0131F13	C 907	9	39.1	44	10	BI518751	BI518751	603061933
C 835	9	39.1	35	12	AZ776709	AZ776709	2M0010N06	C 908	9	39.1	44	12	AZ441185	AZ441185	1M0232001
C 836	9	39.1	35	12	AZ807270	AZ807270	2M0070D04	C 909	9	39.1	44	12	BH170618	BH170618	SALK_0031
C 837	9	39.1	35	12	AZ834104	AZ834104	2M0116G09	C 910	9	39.1	44	12	BH171655	BH171655	SALK_0046
C 838	9	39.1	35	12	AZ984070	AZ984070	2M0265K24	C 911	9	39.1	44	12	BH251020	BH251020	SALK_0108
C 839	9	39.1	35	12	TA181H07Q	TA181H07Q	AL474485 T. brucei	C 912	9	39.1	44	12	BH251583	BH251583	SALK_0118
C 840	9	39.1	36	10	BF339163	BF339163	602038468	C 913	9	39.1	44	12	BH254188	BH254188	SALK_0161
C 841	9	39.1	36	12	AZ974570	AZ974570	2M0249P08	C 914	9	39.1	44	12	BH612745	BH612745	SALK_0332
C 842	9	39.1	36	12	AZ991248	AZ991248	2M0275016	C 915	9	39.1	44	12	BH613346	BH613346	SALK_0341
C 843	9	39.1	37	9	A1520830	A1520830	ti08B09.x	C 916	9	39.1	44	12	BH633361	BH633361	SALK_0421
C 844	9	39.1	37	9	A1574120	A1574120	uj68d12.y	C 917	9	39.1	44	12	BH634038	BH634038	SALK_0439
C 845	9	39.1	37	9	A1641763	A1641763	fc23g04.x	C 918	9	39.1	45	10	BM395809	BM395809	5009-0-12
C 846	9	39.1	37	9	A1755616	A1755616	EteSTea38	C 919	9	39.1	45	12	AZ319010	AZ319010	1M0038I21
C 847	9	39.1	37	9	AA458001	AA458001	vf74g10.r	C 920	9	39.1	45	12	AZ31526	AZ31526	1M0059F04
C 848	9	39.1	37	10	BG166700	BG166700	602339211	C 921	9	39.1	45	12	AZ484343	AZ484343	1M0310D14
C 849	9	39.1	37	10	BF669786	BF669786	603293364	C 922	9	39.1	45	12	AZ503949	AZ503949	1M0343I24
C 850	9	39.1	37	10	BF66183	BF66183	603052811	C 923	9	39.1	45	12	AZ777920	AZ777920	2M0012J13
C 851	9	39.1	37	10	H27436	H27436	y167g07.s1	C 924	9	39.1	45	12	BH212935	BH212935	SALK_0082
C 852	9	39.1	37	12	AQ025713	AQ025713	1(2)k0260	C 925	9	39.1	45	12	BH633155	BH633155	SALK_0403
C 853	9	39.1	37	12	AZ802814	AZ802814	2M0061B21	C 926	9	39.1	45	12	BH633466	BH633466	SALK_0426
C 854	9	39.1	37	12	BH615019	BH615019	BM01854-5	C 927	9	39.1	46	9	AA729084	AA729084	nw03407.r
C 855	9	39.1	38	9	AV837949	AV837949	AV837949	C 928	9	39.1	46	9	AA828199	AA828199	OF05c10.s
C 856	9	39.1	38	10	BG684760	BG684760	602636457	C 929	9	39.1	46	9	AA867748	AA867748	vx1ga12.r
C 857	9	39.1	38	10	BF1859456	BF1859456	603388196	C 930	9	39.1	46	9	AA883189	AA883189	aml8b12.s
C 858	9	39.1	38	10	BM397530	BM397530	5009-0-34	C 931	9	39.1	46	9	AA105291	AA105291	mp36g11.r
C 859	9	39.1	38	10	BF534187	BF534187	601232196	C 932	9	39.1	46	9	AI669413	AI669413	ty32c05.x
C 860	9	39.1	38	12	BH618869	BH618869	SALK_0399	C 933	9	39.1	46	9	AI702349	AI702349	t266b10.x
C 861	9	39.1	39	10	BF978061	BF978061	602147965	C 934	9	39.1	46	9	AA151915	AA151915	z002c08.s
C 862	9	39.1	39	10	BG427606	BG427606	602497043	C 935	9	39.1	46	9	AA206549	AA206549	zq57f01.s
C 863	9	39.1	39	10	BG431624	BG431624	602499216	C 936	9	39.1	46	9	AA833037	AA833037	AV833037
C 864	9	39.1	39	10	BG434687	BG434687	602506777	C 937	9	39.1	46	10	BG115566	BG115566	602317256
C 865	9	39.1	39	10	BG538554	BG538554	602567279	C 938	9	39.1	46	10	BM396739	BM396739	5009-0-24
C 866	9	39.1	39	10	BG542007	BG542007	602572119	C 939	9	39.1	46	10	BF038767	BF038767	601461268
C 867	9	39.1	39	10	BG546916	BG546916	602573906	C 940	9	39.1	46	12	AQ025695	AQ025695	1(2)k0100
C 868	9	39.1	39	10	BG547349	BG547349	602574783	C 941	9	39.1	46	12	AZ991930	AZ991930	2M0276F23
C 869	9	39.1	39	10	BG614605	BG614605	602642087	C 942	9	39.1	47	10	BI916743	BI916743	603178737
C 870	9	39.1	39	10	BG921277	BG921277	602824119	C 943	9	39.1	47	12	BE312415	BE312415	601150971
C 871	9	39.1	39	10	BF1818665	BF1818665	603033263	C 944	9	39.1	47	12	AZ303823	AZ303823	1M0003005
C 872	9	39.1	39	10	BM395803	BM395803	5009-0-12	C 945	9	39.1	47	12	BH213678	BH213678	SALK_0095
C 873	9	39.1	39	10	BF209854	BF209854	601873551	C 946	9	39.1	48	10	BI547258	BI547258	603197123
C 874	9	39.1	39	10	BF213403	BF213403	601845154	C 947	9	39.1	48	10	BI906001	BI906001	603062308
C 875	9	39.1	39	10	BF245648	BF245648	601863581	C 948	9	39.1	48	12	AZ781794	AZ781794	2M0021J21
C 876	9	39.1	39	12	AZ877564	AZ877564	2M0192K05	C 949	9	39.1	48	12	AZ794723	AZ794723	2M0048B01
C 877	9	39.1	39	12	TA32F04Q	TA32F04Q	AL454136 T. brucei	C 950	9	39.1	48	12	AZ929474	AZ929474	479.dif26
C 878	9	39.1	39	12	TA352H03Q	TA352H03Q	AL496533 T. brucei	C 951	9	39.1	48	12	BH625444	BH625444	100710700
C 879	9	39.1	40	9	AA641270	AA641270	nr78a04.s	C 952	9	39.1	49	9	AA657082	AA657082	vs23c09.r
C 880	9	39.1	40	9	AA846437	AA846437	al85c09.s	C 953	9	39.1	49	9	AA934271	AA934271	SMW0J3CAN
C 881	9	39.1	40	9	AA922477	AA922477	om63f09.s	C 954	9	39.1	49	9	AA992903	AA992903	OT92B04.s
C 882	9	39.1	40	9	AI001093	AI001093	os94c01.s	C 955	9	39.1	49	9	AI142280	AI142280	qg63c10.r
C 883	9	39.1	40	9	AA160572	AA160572	2q46d11.r	C 956	9	39.1	49	9	AA146415	AA146415	mr66c08.r
C 884	9	39.1	40	9	AA255159	AA255159	mz82c08.r	C 957	9	39.1	49	9	AI424311	AI424311	te90b05.x
C 885	9	39.1	40	10	BG037009	BG037009	602287258	C 958	9	39.1	49	9	AI434488	AI434488	t145e03.x
C 886	9	39.1	40	10	BG912856	BG912856	602807422	C 959	9	39.1	49	9	AI440059	AI440059	t16f1f10.x
C 887	9	39.1	40	10	T90338	T90338	ye16h01.s1	C 960	9	39.1	49	9	AI453675	AI453675	tj28h04.x
C 888	9	39.1	40	10	BF340179	BF340179	602036555	C 961	9	39.1	49	9	AI652389	AI652389	wb20e07.x
C 889	9	39.1	40	12	AZ802548	AZ802548	2M0061C05	C 962	9	39.1	49	9	AI760858	AI760858	w109b11.x
C 890	9	39.1	40	12	BH633074	BH633074	100706080	C 963	9	39.1	49	9	AI800417	AI800417	tj14b07.x
C 891	9	39.1	41	10	BG251287	BG251287	602366120	C 964	9	39.1	49	9	AI889232	AI889232	wm36b09.x
C 892	9	39.1	41	10	H14824	H14824	ym25d07.s1	C 965	9	39.1	49	10	BG342381	BG342381	602374I08
C 893	9	39.1	41	12	AZ868291	AZ868291	2M0179Q23	C 966	9	39.1	49	10	BI523939	BI523939	603051683

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c 967 9 39.1 49 10 BJ064738 BJ064738
968 9 39.1 49 10 BM176425 TgESTzpb3
969 9 39.1 49 12 AZ472469 1M0387P09
970 9 39.1 49 12 AZ622361 1M0459B09
c 971 9 39.1 49 12 AZ834261 2M0116G19
972 9 39.1 49 12 BH172699
973 9 39.1 49 12 TAG1H08Q
c 974 9 39.1 50 9 AU102278 T. brucei
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ALIGNMENTS

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RESULT 1
BG545479 32 bp mRNA linear EST 04-APR-2001
LOCUS 602572715F1 NIH_MGC_77 Homo sapiens cDNA clone IMAGE:4701099 5',
DEFINITION mRNA sequence.
ACCESSION BG545479
VERSION BG545479.1 GI:13544144
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE NIH-MGC http://mgc.nci.nih.gov/
JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgabs-f@mail.nih.gov
Tissue Procurement: CLONTECH Laboratories, Inc.
cDNA Library Preparation: CLONTECH Laboratories, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: L1CM1535 row: m column: 04
High quality sequence stop: 32.
FEATURES
source Location/Qualifiers
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/db_xref="taxon:9606"
/clone="IMAGE:4701099"
/clone_lib="NIH_MGC_77"
/lab_host="DH10B (T1 phage-resistant)"

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/notes="Organ: lung; Vector: pDNR-LIB (Clontech); Site_1:
SfiI (ggcgctcgcc); Site_2: SfiI (ggcattatggcc); 5' and
3' adaptors were used in cloning as follows: 5' adaptor
sequence: 5'-CACGGCCATTATGGCC-3' and 3' adaptor sequence:
5'-ATTCTAGAGCCGAGCGGCGGACATG-dT(30)BN-3' (where B = A,
C, or G and N = A, C, G, or T). Average insert size 1.9
kb (range 0.5-4.0 kb). 12/15 colonies contained inserts
by PCR. This library was enriched for full-length clones
and was constructed by Clontech Laboratories (Palo Alto,
CA). Note: this is a NIH_MGC Library."
BASE COUNT 5 a 10 c 13 g 4 t
ORIGIN

Query Match 62.6%; Score 14.4; DB 10; Length 32;
Best Local Similarity 93.8%; Pred. No. 9.3e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 ccaggcgctcgtctggg 17
|||||
Db 14 CCAGCGCTCTCGGGG 29

RESULT 2
AU106915 50 bp mRNA linear EST 30-AUG-2001
LOCUS AU106915 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
DEFINITION HEP05791, mRNA sequence.
ACCESSION AU106915
VERSION AU106915.1 GI:13556436
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE Diverse transcriptional initiation revealed by fine, large-scale
mapping of mRNA start sites
JOURNAL EMBO Rep. 2 (5), 388-393 (2001)
MEDLINE 21270072
COMMENT Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: ysuzukl@ims.u-tokyo.ac.jp
Suzuki, Y., Yoshimoto-Nakagawa, K., Maruyama, K., Suyama, A. and Sugano
, S. Construction and characterization of a full length-enriched and
a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).
FEATURES
source Location/Qualifiers
1..50
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="HEP05791"
/clone_lib="Sugano Homo sapiens cDNA library"
BASE COUNT 7 a 12 c 21 g 10 t
ORIGIN

Query Match 60.9%; Score 14; DB 9; Length 50;
Best Local Similarity 77.3%; Pred. No. 1.6e+04;
Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 2 ccaggcgctcgtctgggcacat 23
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Db 14 CCTGGCGTCTGCTGGGGCACCT 35

RESULT 3
AU097023 34 bp mRNA linear EST 20-AUG-1998
LOCUS AU097023

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DEFINITION      oz22e03.x1 Soares_total_fetus_Nb2HF8_9w Homo sapiens cDNA clone
IMAGE:1676092 3' similar to TR:015141 O15141 DAXX ;, mRNA sequence.
ACCESSION       AI097023
VERSION         AI097023.1 GI:3446605
KEYWORDS        EST.
SOURCE          human.
ORGANISM        Homo sapiens
                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
REFERENCE       1 (bases 1 to 34)
AUTHORS         NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE           National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                Tumor Gene Index
                Unpublished (1997)
                Contact: Robert Strausberg, Ph.D.
                Email: cgabs-r@mail.nih.gov
                This clone is available royalty-free through LLNL : contact the
                IMAGE Consortium (info@image.llnl.gov) for further information.
                Seq primer: -40ml3 fwd. ET from Amersham
                High quality sequence stop: 1.
FEATURES        Location/Qualifiers
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                /clone="IMAGE:1676092"
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                /lab_host="DH10B"
                /note="Vector: pT7T3D-Pac (Pharmacia) with a modified
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                was prepared from mRNA obtained from pooled 8-9 week
                (total) fetus material with a Not I - oligo(dT) primer [5',
                TGTTCACCAATCTGAAGTGGGAGCGCGCTTAATTTTCTTTTCTTTT 3'].
                Double-stranded cDNA was ligated to Eco RI adaptors
                (Pharmacia), digested with Not I and cloned into the Not I
                and Eco RI sites of the modified pT73 vector. Library
                went through one round of normalization, and was
                constructed by Bento Soares and M. Fatima Bonaldo. "
BASE COUNT      6 a      8 c      7 g      13 t
ORIGIN
Query Match     59.1%; Score 13.6; DB 9; Length 34;
Best Local Similarity 80.0%; Pred. No. 2.1e+04;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 4 aggcgtctcgtggccacat 23
||||| || ||||| ||
Db 2 AGCGTTTCTCGGGGCATAT 21

RESULT 4
AI537615/c
LOCUS           AI537615
DEFINITION      tp05d08.x1 NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2186895 3'
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ACCESSION       AI537615
VERSION         AI537615.1 GI:4451750
KEYWORDS        EST.
SOURCE          human.
ORGANISM        Homo sapiens
                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
REFERENCE       1 (bases 1 to 34)
AUTHORS         NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE           National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                Tumor Gene Index
                Unpublished (1997)
                Contact: Robert Strausberg, Ph.D.
                Email: cgabs-r@mail.nih.gov
                Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
                Emmert-Buck, M.D., Ph.D.
                cDNA Library Preparation: Life Technologies, Inc.

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CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www.bio.llnl.gov/bbrp/image/image.html

Trace considered overall poor quality
Seq primer: -40UP from Gibco
High quality sequence stop: 1.
FEATURES        Location/Qualifiers
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                /clone_lib="NCI_CGAP_Gas4"
                /tissue_type="poorly differentiated adenocarcinoma with
                signet ring cell features"
                /lab_host="DH10B"
                /note="Organ: stomach; Vector: pCMV-SPORT6; Site_1: SalI;
                Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT.
                Average insert size 1.69 kb. Life Technologies catalog #:
                11549-011"
BASE COUNT      6 a      16 c      12 g      0 t
ORIGIN
Query Match     57.4%; Score 13.2; DB 9; Length 34;
Best Local Similarity 83.3%; Pred. No. 3.2e+04;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

.QY 2 ccaggcgtctcgtggccc 19
||||| || ||||| ||||
Db 19 CCCGGGTCCTCGTGGCC 2

RESULT 5
AU102952
LOCUS           AU102952
DEFINITION      AU102952 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
                COLFI788, mRNA sequence.
ACCESSION       AU102952.1 GI:13552473
VERSION         AU102952.1
KEYWORDS        EST.
SOURCE          human.
ORGANISM        Homo sapiens
                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
REFERENCE       1 (bases 1 to 50)
AUTHORS         Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J., Hata
                ,H., Ota,T., Isogai,T., Tanaka,T., Morishita,S., Okubo,K., Sakaki
                ,Y., Nakamura,Y., Suyama,A. and Sugano,S.
                Diverse transcriptional initiation revealed by fine, large-scale
                mapping of mRNA start sites
                EMBO Rep. 2 (5), 388-393 (2001)
                21270072
                Contact: Yutaka Suzuki
                Department of Virology
                Institute of Medical Science, University of Tokyo
                4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
                Email: ysuzuki@ims.u-tokyo.ac.jp
                Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and Sugano
                ,S. Construction and characterization of a full length-enriched and
                a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).
FEATURES        Location/Qualifiers
                1..50
                /organism="Homo sapiens"
                /db_xref="taxon:9606"
                /clone="COLFI788"
                /clone_lib="Sugano Homo sapiens cDNA library"
BASE COUNT      17 a      11 c      16 g      6 t
ORIGIN

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```

Query Match      57.4%; Score 13.2; DB 9; Length 50;
Best Local Similarity 83.3%; Pred. No. 3.6e+04;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 6 gcgtctcgtggccacat 23
    ||||| ||||| |||||
Db 33 GAGTATCGCGGCCACAT 50

RESULT 6
LOCUS AU106296/c
DEFINITION AU106296 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
            KAT06033, mRNA sequence.
ACCESSION AU106296
VERSION AU106296.1 GI:13555817
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 50)
AUTHORS Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J., Hata
            ,H., Ota,T., Isogai,T., Tanaka,T., Morishita,S., Okubo,K., Sakaki
            ,Y., Nakamura,Y., Suyama,A. and Sugano,S.
            Diverse transcriptional initiation revealed by fine, large-scale
            mapping of mRNA start sites
JOURNAL EMBO Rep. 2 (5), 388-393 (2001)
MEDLINE 21270072
COMMENT Contact: Yutaka Suzuki
            Department of Virology
            Institute of Medical Science, University of Tokyo
            4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
            Email: yzuku@iems.u-tokyo.ac.jp
Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and Sugano
            ,S. Construction and characterization of a full length-enriched and
            a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).

FEATURES
    source
        1..50
        /organism="Homo sapiens"
        /db_xref="taxon:9606"
        /clone="KAT06033"
        /clone_lib="Sugano Homo sapiens cDNA library"
BASE COUNT 12 a 11 c 16 g 11 t
ORIGIN

Query Match      57.4%; Score 13.2; DB 9; Length 50;
Best Local Similarity 83.3%; Pred. No. 3.6e+04;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 accaggcgtctcgtgggc 18
    ||||| ||||| |||||
Db 30 ACAAGGCTCTCTTGTC 13

RESULT 7
LOCUS T64778/c
DEFINITION T64778 44 bp mRNA linear EST 20-FEB-1995
            YC25h10.r1 Stratagene liver (#937224) Homo sapiens cDNA clone
            IMAGE:81763 5', similar to gb:M14058 COMPLEMENT CIR COMPONENT
            PRECURSOR (HUMAN);, mRNA sequence.
ACCESSION T64778
VERSION T64778.1 GI:673823
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 44)
AUTHORS Hillier,L., Lennon,G., Becker,M., Bonaldo,M.F., Chitapelli,B.,
            Chisoe,S., Dietrich,N., Dubuque,T., Favello,A., Gish,W., Hawkins
            ,M., Hultman,M., Kucaba,T., Lacy,M., Le,M., Le,N., Mardis,E., Moore

B., Morris,M., Parsons,J., Prange,C., Rifkin,L., Rohlfing,T.,
Schellenberg,K., Soares,B.B., Tan,F., Thierry-Mieg,J., Trevaskis,E.,
Underwood,K., Wohlmann,P., Waterston,R., Wilson,R. and Marra,M.
Generation and analysis of 280,000 human expressed sequence tags
Genome Res. 6 (9), 807-828 (1996)
9704478
Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: estewatson.wustl.edu
Insert Size: 57
High quality sequence starts: 1 High quality sequence stops: 1
Source: IMAGE Consortium, LLNL This clone is available royalty-free
through LLNL : contact the IMAGE Consortium (info@image.llnl.gov)
for further information. Trace considered overall poor quality
Insert Length: 57 Std Error: 0.00
Seq primer: M13RP1
High quality sequence stop: 1.
FEATURES
    source
        1..44
        /organism="Homo sapiens"
        /db_xref="GDB:498820"
        /db_xref="taxon:9606"
        /clone="IMAGE:81763"
        /clone_lib="Stratagene liver (#937224)"
        /sex="male"
        /dev_stage="49 years old"
        /lab_host="SOLR cells (kanamycin resistant)"
        /note="Organ: liver; Vector: pBluescript SK; Site_1: EcoRI
            ; Site_2: XhoI; Cloned unidirectionally. Primer: Oligo
            dt. Hepatectomy from normal male caucasian. Average insert
            size: 1.1 kb; Uni-ZAP XR Vector: -5' adaptor sequence: 5'
            GAATTCGGCAG 3' -3' adaptor sequence: 5'
            CTCGAGTTTTTTTTTTTTTTT 3'"
BASE COUNT 5 a 13 c 12 g 11 t 3 others
ORIGIN

Query Match      56.5%; Score 13; DB 10; Length 44;
Best Local Similarity 59.6%; Pred. No. 4.3e+04;
Matches 16; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 1 accaggcgtctcgtggccacat 23
    ||||| | | |||||
Db 37 ACCAGGAGNNACAGGCCACAT 15

RESULT 8
LOCUS BM395935
DEFINITION BM395935 32 bp mRNA linear EST 17-JAN-2002
            Tetrahymena thermophila cDNA, mRNA sequence.
ACCESSION BM395935
VERSION BM395935.1 GI:18195988
KEYWORDS EST.
SOURCE Tetrahymena thermophila.
ORGANISM Tetrahymena thermophila
            Eukaryota; Alveolata; Ciliophora; Oligohymenophorea;
            Hymenostomatida; Tetrahymenina; Tetrahymena.
REFERENCE 1 (bases 1 to 32)
AUTHORS Turkewitz,A.P., Karrer,K.M., Jahn,C., Orlas,E., Kirk,K.E., Frankel
            ,J. and Klobutcher,L.
            EST from Tetrahymena thermophila, strain CU428.1, growing cells
            from Tetrahymena thermophila.
            Unpublished (2002)
Contact: Turkewitz AP
Molecular Genetics and Cell Biology
University of Chicago
920 E. 58th Street, Chicago, IL 60637, USA
Tel: 773 702 4374
Fax: 773 702 3172
Email: apturkew@midway.uchicago.edu

```

```

FEATURES
Source
Seq primer: T3.
Location/Qualifiers
1..32
/organism="Tetrahymina thermophila"
/db_xref="taxon:5911"
/clone_lib="Chilcoat/Turkewitz cDNA (large fraction)"
/note="Vector: Bluescript2 SK+; Details on library
preparation can be found in Chilcoat and Turkewitz (2001)
Proc. Natl. Acad. Sci USA, 98: 8709-8713."
BASE COUNT      4 a      13 c      11 g      4 t
ORIGIN

Query Match      54.8%; Score 12.6; DB 10; Length 32;
Best Local Similarity 78.9%; Pred. No. 5.8e+04;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 accaggcgtctcgtgggcc 19
||||| ||||| |||||
Db 7 ACCACGCGTGGCGTGCC 25

RESULT 9
AI685223
LOCUS      wc70e01.x1 NCI_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2323992 3'
DEFINITION similar to SW:GC3_HUMAN P01860 IG GAMMA-3 CHAIN C REGION ;, mRNA
sequence.
ACCESSION AI685223
VERSION    AI685223.1 GI:4896517
KEYWORDS   EST.
SOURCE     human.
ORGANISM   Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 43)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Life Technologies catalog #: 11548-013
DNA Sequencing by: Washington University Genome Sequencing Center
Clone Distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Trace considered overall poor quality
Insert Length: 815 Std Error: 0.00
Seq primer: -40UP from Gibco
High quality sequence stop: 1.
Location/Qualifiers
1..43
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2323992"
/clone_lib="NCI_CGAP_Pan1"
/tissue_type="adenocarcinoma"
/lab_host="DH10B"
/note="Organ: pancreas; Vector: pCMV-SPORT6; Site_1: SalI;
Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.72 kb. Life Technologies catalog #:
11548-013"
BASE COUNT      11 a      11 c      19 g      2 t
ORIGIN

Query Match      54.8%; Score 12.6; DB 9; Length 43;
Best Local Similarity 78.9%; Pred. No. 6.4e+04;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

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```

QY 1 accaggcgtctcgtgggcc 19
||||| ||||| |||||
Db 24 ACCAGGATCTCGGGGCC 42

RESULT 10
AI106914
LOCUS      AU106914 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
DEFINITION CAS07931, mRNA sequence.
ACCESSION AU106914
VERSION    AU106914.1 GI:13556435
KEYWORDS   EST.
SOURCE     human.
ORGANISM   Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 50)
Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J., Hata
,H., Ota,T., Isogai,T., Tanaka,T., Morishita,S., Okubo,K., Sakaki
,Y., Nakamura,Y., Suyama,A. and Sugano,S.
Diverse transcriptional initiation revealed by fine, large-scale
mapping of mRNA start sites
EMBO Rep. 2 (5), 388-393 (2001)
21270072
Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: ysuzuki@ims.u-tokyo.ac.jp
Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and Sugano
,S. Construction and characterization of a full length-enriched and
a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).
Location/Qualifiers
1..50
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="CAS07931"
/clone_lib="Sugano Homo sapiens cDNA library"
BASE COUNT      9 a      11 c      22 g      8 t
ORIGIN

Query Match      54.8%; Score 12.6; DB 9; Length 50;
Best Local Similarity 78.9%; Pred. No. 6.7e+04;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 5 ggcgtctcgtgggccacat 23
||||| ||||| |||||
Db 13 GGCCTCTGCTGGGGCACCT 31

RESULT 11
AI106917
LOCUS      AU106917 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
DEFINITION HRC07960, mRNA sequence.
ACCESSION AU106917
VERSION    AU106917.1 GI:13556438
KEYWORDS   EST.
SOURCE     human.
ORGANISM   Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 50)
Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J., Hata
,H., Ota,T., Isogai,T., Tanaka,T., Morishita,S., Okubo,K., Sakaki
,Y., Nakamura,Y., Suyama,A. and Sugano,S.
Diverse transcriptional initiation revealed by fine, large-scale
mapping of mRNA start sites
EMBO Rep. 2 (5), 388-393 (2001)
21270072
Contact: Yutaka Suzuki

```

Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: yusuzuki@ims.u-tokyo.ac.jp
Suzuki, Y., Yoshitomo-Nakagawa, K., Maruyama, K., Suyama, A. and Sugano
S. Construction and characterization of a full length-enriched and
a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).

FEATURES

source
1. .50
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="HRC07960"
/clone_lib="Sugano Homo sapiens cDNA library"
8 a 11 c 23 g 8 t

BASE COUNT

Query Match 54.8%; Score 12.6; DB 9; Length 50;
Best Local Similarity 78.9%; Pred. No. 6.7e+04;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 5 ggcgtctcgtgggccacat 23
||||| ||||| |||||
Db 14 GGCCTCTCTGGGGCACCT 32

RESULT 12

AU106918
LOCUS AU106918 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
DEFINITION HSI04186, mRNA sequence.

ACCESSION AU106918
VERSION AU106918.1 GI:13556439
KEYWORDS EST.
SOURCE human.

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE

AUTHORS Suzuki, Y., Taira, H., Tsunoda, T., Mizushima-Sugano, J., Sese, J., Hata
H., Ota, T., Isogai, T., Tanaka, T., Morishita, S., Okubo, K., Sakaki
Y., Nakamura, Y., Suyama, A. and Sugano, S.
Diverse transcriptional initiation revealed by fine, large-scale
mapping of mRNA start sites

JOURNAL EMBO Rep. 2 (5), 388-393 (2001)
MEDLINE 21270072
COMMENT

Contact: Yutaka Suzuki

Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: yusuzuki@ims.u-tokyo.ac.jp

Suzuki, Y., Yoshitomo-Nakagawa, K., Maruyama, K., Suyama, A. and Sugano
S. Construction and characterization of a full length-enriched and
a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).

FEATURES

source
1. .50
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="HSI04186"
/clone_lib="Sugano Homo sapiens cDNA library"
7 a 10 c 24 g 9 t

BASE COUNT

Query Match 54.8%; Score 12.6; DB 9; Length 50;
Best Local Similarity 78.9%; Pred. No. 6.7e+04;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 5 ggcgtctcgtgggccacat 23
||||| ||||| |||||
Db 16 GGCCTCTCTGGGGCACCT 34

RESULT 13

AU106920
LOCUS AU106920 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
DEFINITION HSI05986, mRNA sequence.

ACCESSION AU106920
VERSION AU106920.1 GI:13556441
KEYWORDS EST.
SOURCE human.

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE

AUTHORS Suzuki, Y., Taira, H., Tsunoda, T., Mizushima-Sugano, J., Sese, J., Hata
H., Ota, T., Isogai, T., Tanaka, T., Morishita, S., Okubo, K., Sakaki
Y., Nakamura, Y., Suyama, A. and Sugano, S.

Diverse transcriptional initiation revealed by fine, large-scale
mapping of mRNA start sites

JOURNAL EMBO Rep. 2 (5), 388-393 (2001)
MEDLINE 21270072
COMMENT

Contact: Yutaka Suzuki

Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: yusuzuki@ims.u-tokyo.ac.jp

Suzuki, Y., Yoshitomo-Nakagawa, K., Maruyama, K., Suyama, A. and Sugano
S. Construction and characterization of a full length-enriched and
a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).

FEATURES

source
1. .50
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="HSI05986"
/clone_lib="Sugano Homo sapiens cDNA library"
7 a 10 c 24 g 9 t

BASE COUNT

Query Match 54.8%; Score 12.6; DB 9; Length 50;
Best Local Similarity 78.9%; Pred. No. 6.7e+04;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 5 ggcgtctcgtgggccacat 23
||||| ||||| |||||
Db 16 GGCCTCTCTGGGGCACCT 34

RESULT 14

AZ789608/c
LOCUS AZ789608 50 bp DNA linear GSS 16-FEB-2001
DEFINITION 2M0037L01R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC2M0037L01 R, DNA sequence.

ACCESSION AZ789608
VERSION AZ789608.1 GI:12930609
KEYWORDS GSS.
SOURCE house mouse.

ORGANISM

Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE

AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly
M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A.
and Wright, D., Weiss, R.

Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

JOURNAL

COMMENT Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 595 5606

Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0037 row: L column: 01
Seq primer: CACACAGGAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 50.
Location/Qualifiers

FEATURES

source

1. .50
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0037L01"
/clone_lib="Mouse 10kb plasmid UUGCLM library"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/note="Vector: PWD42nv; Purified genomic DNA from M.
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gil4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

BASE COUNT
ORIGIN

13 a 17 c 12 g 8 t

Query Match 54.8%; Score 12.6; DB 12; Length 50;

Best Local Similarity 78.9%; Pred. No. 6.7e+04;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 3 caggcgctctcggtggccac 21

||||| ||||| |||||

Db 27 CTGGCCTGCTGGGCCCC 9

RESULT 15

AZ309417

LOCUS

1M0013G12R Mouse 10kb plasmid UUGCLM library Mus musculus genomic
clone UUGCLM0013G12 R, DNA sequence.

DEFINITION

Accession

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Contact: Robert B. Weiss

University of Utah

Rm. 308, Biomedical

84112, USA

Mouse whole genome scaffolding with paired end reads from 10kb

plasmid inserts

Unpublished (2000)

University of Utah

Genome Center

20 S. 2030 E., SLC, UT

84112, USA

Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0013 row: G column: 12
Seq primer: CACACAGGAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 38.
Location/Qualifiers

FEATURES

source

1. .38
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGCLM0013G12"
/clone_lib="Mouse 10kb plasmid UUGCLM library"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/note="Vector: PWD42nv; Purified genomic DNA from M.
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gil4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

BASE COUNT
ORIGIN

8 a 13 c 13 g 4 t

Query Match 53.9%; Score 12.4; DB 12; Length 38;

Best Local Similarity 72.7%; Pred. No. 7.5e+04;
Matches 16; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 2 ccaggcgctctcggtggccacat 23

||||| ||||| |||||

Db 14 CCGGGCCTGACCTGGGGCACAT 35

Search completed: August 17, 2002, 23:24:27

Job time: 7012 sec

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